

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 14:34:12 ; Search time 193 Seconds

(without alignments)
193.779 Million cell updates/sec

Title: US-10-272-121-2

Perfect score: 357

Sequence: 1 MRHYLLFALLFLVLPVPG.....LPKEDQIGKSTRGRKCR 65

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt 02:*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	357	100.0	67	1 D103_HUMAN	P81534 homo sapien
2	353	98.9	67	2 Q7PCK4	Q7PCK4 papio anubi
3	349	97.8	64	1 D103_PANTR	Q951d2 pan troglod
4	302	84.6	67	1 BD01_CHILA	P83943 chinchilla
5	298	83.5	67	2 O6SC68	O6SC68 sus scrofa
6	298	83.5	67	2 AAR88759	AAR88759 sus scrofa
7	256	71.7	67	2 Q7TNV9	Q7TNV9 mus musculu
8	143	40.1	64	2 O6E5P6	O6E5P6 equus cabal
9	135	37.8	64	1 BD02_PANTR	Q9t112 pan troglod
10	134	37.5	64	1 BD02_MACMU	Q9pds9 macaca mula
11	133	37.3	64	1 BD02_HUMAN	A13263 homo sapien
12	133	37.3	64	2 AAR69285	AAR69285 homo sapi
13	116.5	32.6	63	1 BD03_MOUSE	Q9wcl0 mus musculu
14	116	32.5	64	1 EAP_BOVIN	Q02775 bos taurus
15	115	32.2	60	2 Q7IUD5	Q7IUD5 bos taurus
16	115	32.2	60	2 AAD43032	AAD43032 bos tauru
17	114	31.9	64	1 BD01_PIG	O62697 sus scrofa
18	108	30.3	64	1 LAP_BOVIN	Q28880 bos taurus
19	108	30.3	65	1 MYX1_CRODU	P24331 croctatus du
20	108	30.3	65	1 MYX3_CRODU	P24333 croctatus du
21	106	29.7	64	1 BD05_BOVIN	P46163 bos taurus
22	106	29.7	64	1 TAP_BOVIN	P25068 bos taurus
23	105	29.4	65	2 Q9PMF3	Q9PMF3 croctatus du
24	103	28.9	65	2 O57540	O57540 croctatus du
25	102	28.6	71	2 O91V70	O91V70 mus musculu
26	101	28.3	63	2 O6TMH5	O6TMH5 bubalus bub
27	101	28.3	63	2 AAO93463	AAO93463 bubalus bub
28	101	28.3	64	2 Q7Y843	Q7Y843 capra hircu
29	100	28.0	64	2 O97942	O97942 capra hircu
30	96.5	27.0	80	2 Q9D658	Q9D658 gallus gall
31	96	26.9	64	2 Q73799	Q73799 croctatus du

ALIGNMENTS

32	95.5	26.8	63	1	BD02_RAT	O88514 rattus norv
33	95	26.6	64	1	BD01_CAPI	O97946 capra hircu
34	95	26.6	64	1	BD02_SHEP	O19039 ovis aries
35	94	26.3	53	1	BD07_BOVIN	O18815 bos taurus
36	94	26.3	64	2	Q9EPV9	Q9EPV9 mus musculu
37	93.5	26.2	63	2	Q9IVD6	Q9IVD6 mus musculu
38	93.5	26.2	80	2	O6GXJ2	O6GXJ2 gallus gall
39	93	26.1	60	2	O8R556	O8R556 mus musculu
40	92	25.8	60	2	Q9IV82	Q9IV82 mus musculu
41	92	25.8	63	1	BD04_BOVIN	P20169 mus musculu
42	90.5	25.4	59	1	BD04_MOUSE	Q90571 melagris s
43	89.5	25.1	63	2	Q9DGS7	P46164 bos taurus
44	89	24.9	42	1	BD06_BOVIN	O89117 rattus norv
45	89	24.9	69	1	BD01_RAT	

RESULT 1

ID D103_HUMAN STANDARD; PRT; 67 AA.

AC P81534; Q8NPG6; Q9NPF6;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 45, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE Beta-defensin 103a precursor (Beta-defensin 3) (DEFB-3) (BD-3) (HBD-3) (HBD3) (Defensin like protein).

GN Name=DEFB103a; Synonyms=DEFB103, DEFB3, BD3;

OS Homo sapiens (Human);

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OC NCBI_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A., SEQUENCE OF 23-67, FUNCTION, TISSUE SPECIFICITY,

RP INDUCTION, AND MASS SPECTROMETRY.

RC TISSUE=keratinocytes, lung epithelial cells, and tracheal epithelium;

RX MEDLINE=21101950; PubMed=11085590; DOI=10.1074/jbc.M00855200;

RA Harder J., Barrels U., Christophers E., Schroeder J.-M.,

RT Isolation and characterization of human beta-defensin-3, a novel

RT human inducible peptide antibiotic.";

RL J. Biol. Chem. 276:5707-5713(2001).

RN [2]

RP SEQUENCE FROM N.A., AND CHARACTERIZATION.

RX MEDLINE=2158153; PubMed=11702237; DOI=10.1007/s004410100433;

RA Conejo-Garcia J.-R., Taubman F., Schuit S., Krause A.,

RA Rodriguez-Vimenez J., Forssman U., Adernan K., Kluever E.,

RA Vogelemeier C., Becker D., Hedrich R., Forssman W.-G., Bals R.,

RT Identification of a novel, multifunctional beta-defensin (human beta-

RT defensin 3) with specific antimicrobial activity. Its interaction with

RT plasma membranes of Xenopus oocytes and the induction of macrophage

RT chemotaxis.";

RL Cell Tissue Res. 306:257-264(2001).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=21125233; PubMed=11223260; DOI=10.1016/S0378-1119(00)00569-2;

RA Jia H.P., Schutte B.C., Schudy A., Linzmeier R., Guthmiller J.M.,

RA Johnson G.K., Tack B.F., Mitros J.P., Rosenthal A., Ganz T.,

RA McTay P.B. Jr.,

RT Discovery of new human defensins using a genomics-based approach.";

RL Gene 263:211-218(2001).

RN [4]

RP SEQUENCE FROM N.A.

RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

RL [5]

RP SEQUENCE FROM N.A.

RA Adler D.A., Diamond G., Sheppard P., Hollway J., Presnell S.,

RA Jaepers S., Whitmore T., Fox B., Gosink U., Rixon M., Gao Z.,

RA Haldeman B., O'Hara P.,

RT EST and genomic database mining yield novel human and mouse beta-

RT defensins.";

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Tonsil;
 RA Chen S., He P., Li R.;
 RT "Cloning and expression of Chinese human beta defensin-3";
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP STRUCTURE BY NMR OF 23-67.
 RX MEDLINE=21864161; PubMed=11741980; DOI=10.1074/jbc.M108302007;
 RA Schilli D.J., Hunter H.N., Aseyev V., Starnes T.D., Wiencek J.M.,
 MCGray P.B. Jr., Tack B.F., Vogel H.J.;
 RT "The solution structures of the human beta-defensins lead to a better
 understanding of the potent bactericidal activity of HBD3 against
Staphylococcus aureus.";
 RL J. Biol. Chem. 277:8279-8289(2002).
 CC -1- FUNCTION: Exhibits antimicrobial activity against Gram-positive
 bacteria *S. aureus* and *S. pyogenes*, Gram-negative bacteria
P. aeruginosa and *E. coli* and the yeast *C. albicans*. Kills
 multi-resistant *S. aureus* and vancomycin-resistant *E. faecium*. No
 significant hemolytic activity was observed.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Highly expressed in skin and tonsils, and to a
 lesser extent in trachea, uterus, kidney, thymus, adenoid, pharynx
 and tongue. Low expression in salivary gland, bone marrow, colon,
 stomach, polyp and larynx. No expression in small intestine.
 CC -1- INDUCTION: By infection of bacteria and by interferon gamma.
 CC -1- MASS SPECTROMETRY: MW=5154.59; METHOD=Electrospray; RANGE=23-67;
 CC NOTE=Ref.1.
 CC -1- SIMILARITY: Belongs to the beta-defensin family.
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 CC -----
 DR EMBL: AJ237673; CAC03097.1; -;
 DR EMBL: AF295370; AAG02237.1; -;
 DR EMBL: AF217245; AAF73853.1; -;
 DR EMBL: AB037872; BAB0572.1; -;
 DR EMBL: AF301870; AAG22030.1; -;
 DR EMBL: AF516673; AAM62424.1; -;
 DR PDB: 1KU6; NMR; A=23-66.
 DR Genew; HGNC:15967; DEFB103A.
 DR MIM; 606611; -;
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0006965; P:anti-Gram-positive bacterial polypeptide in...; TAS.
 DR InterPro; IPR001855; Defensin_beta.
 DR Pfam; PF00711; Defensin_beta.1.
 KW 3D-structure; Antibiotic; Direct protein sequencing; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 67 Beta-defensin 103A.
 FT DISULFID 33 62
 FT DISULFID 40 55
 FT DISULFID 45 63
 FT CONFLICT 45 45 C -> R (in Ref. 6).
 FT TURN 29 31
 FT TURN 32 36
 FT STRAND 39 41
 FT STRAND 47 48
 FT STRAND 49 53
 FT STRAND 61 65
 SQ SEQUENCE 67 AA; 7697 MW; 54266DE1C90D4B65 CRC64;
 Query Match 100.0%; Score 357; DB 1; Length 67;
 Best Local Similarity 100.0%; Pred. No. 6, 3e-34;
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRHYLLFALLFLFLVVPVPGHGIINTLQKYCYRVRGRCVAVLSCLPKREQIGKSTGR 60
 DB 1 MRHYLLFALLFLFLVVPVPGHGIINTLQKYCYRVRGRCVAVLSCLPKREQIGKSTGR 60

QY 61 KCCR 65
 DB 61 KCCR 65
 RESULT 2
 ID Q7PCK4 PRELIMINARY; PRT; 67 AA.
 AC Q7PCK4
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE DEFB103-like protein (Fragment).
 OS *Papio anubis* (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Papio.
 OX NCBI_TaxID=9555;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22619651; PubMed=12734011;
 RA Sempke C.A., Rolfe M., Dorin J.R.;
 RT "Duplication and selection in the evolution of primate beta-defensin
 genes.";
 RL Genome Biol. 4:R31-R31(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Sempke C.A.M., Rolfe M., Dorin J.R.;
 RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- MISCELLANEOUS: The sequence shown here is derived from an
 EMBL/GenBank/DBJ third party annotation (TPA) entry.
 DR EMBL: BK000557; DA01350.1;
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0006613; P:response to pest/pathogen/parasite; IEA.
 DR InterPro; IPR001855; Defensin_beta.
 DR Pfam; PF00711; Defensin_beta.1.
 FT NON TER 67
 SQ SEQUENCE 67 AA; 7669 MW; 543F50570B5D4B65 CRC64;
 Query Match 98.9%; Score 353; DB 2; Length 67;
 Best Local Similarity 98.5%; Pred. No. 1, 9e-33;
 Matches 64; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MRHYLLFALLFLFLVVPVPGHGIINTLQKYCYRVRGRCVAVLSCLPKREQIGKSTGR 60
 DB 1 MRHYLLFALLFLFLVVPVPGHGIINTLQKYCYRVRGRCVAVLSCLPKREQIGKSTGR 60
 QY 61 KCCR 65
 DB 61 KCCR 65
 RESULT 3
 ID D103_PANTR STANDARD; PRT; 64 AA.
 AC D103_PANTR
 DT 28-MAR-2004 (rel. 43, Created)
 DT 28-MAR-2004 (rel. 43, Last sequence update)
 DT 05-JUL-2004 (rel. 44, Last annotation update)
 DE Beta-defensin 103A precursor (Beta-defensin 3) (DEFB-3) (BD-3)
 DE (Fragment).
 GN Name=DEFB103A; Synonyms=DEFB3, DEFB3;
 OS *Pan troglodytes* (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.
 OX NCBI_TaxID=9596;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Ditts L.A., Langemann J.A.M., Ravenbergen B., Paltansing S.,
 Verweene R.A.W., Hienstra P.S., Thomas A.W., Nibbering P.H.;

RT "Expression of chimpanzee (Pan troglodytes) beta-defensin-3";
 RI Submitted (May-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Exhibits antimicrobial activity against Gram-positive
 CC and Gram-negative bacteria (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the beta-defensin family.
 CC -----
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 CC -----
 CC DR EMBL; AY033883; AAK61549.1; -
 DR InterPro; IPR001855; Defensin_beta.
 DR Pfam; PF00711; Defensin_beta; 1.
 KW Antibiotic; Signal.
 FT SIGNAL 1 22 By similarity.
 FT CHAIN 23 >64 Beta-defensin 103A.
 FT DISULFID 33 62 By similarity.
 FT DISULFID 40 55 By similarity.
 FT DISULFID 45 63 By similarity.
 FT NON TER 64 64
 SQ SEQUENCE 64 AA; 7299 MW; 01C90D4B60218DC8 CRC64;
 Query Match 97.8%; Score 349; DB 1; Length 64;
 Best Local Similarity 98.4%; Pred. No. 5.3e-33;
 Matches 63; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRIHYLLFALLFLFVLPVPGHGIIINTLOKYYCVRVGRCAVLSCLPKREQIGKSTRGR 60
 DB 1 MRIHYLLFALLFLFVLPVPGHGIIINTLOKYYCVRVGRCAVLSCLPKREQIGKSTRGR 60
 QY 61 KCCR 64
 DB 61 KCCR 64
 Db 61 KCCR 64
 RESULT 4
 B001 CHILA STANDARD; PRT; 67 AA.
 ID PD3943;
 AC PD3943;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Beta-defensin 1 precursor (CBD-1).
 GN Name=DEFB1; Synonyms=BD1;
 OS Chinchilla lanigera (Chinchilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathu; Chinchillidae;
 OC Chinchilla.
 OC NCBI_TaxID=34839;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND MASS
 RP SPECTROMETRY.
 RA TISSUE= tongue, and Trachea;
 RX PubMed=1496845; DOI=10.1074/jbc.M400499200.
 RT Harris R.H., Milk D., Bevins C.L., Munson R.S. Jr., Bakaletz L.O.;
 RT "Identification and characterization of mucosal antimicrobial peptides
 RT expressed by the chinchilla (Chinchilla lanigera) airway.";
 RL J. Biol. Chem. 279:20250-20256(2004).
 CC -1- FUNCTION: Has antibacterial activity against Gram-positive
 CC bacterium S. pneumoniae Serotype 14. Is also active against Gram-
 CC negative bacteria M. catarrhalis 1857, and nontypeable H. influenzae
 CC strains 86-028NP and 1128. Has antifungal activity against
 CC C. albicans. May have a role in maintaining sterility in the middle
 CC ear.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Highly expressed in tongue, nasopharyngeal
 CC mucosa and skin, and to a lower extent in the Eustachian tube,
 CC lung and trachea.

CC -1- MASS SPECTROMETRY: MW=5123; METHOD=Electrospray; RANGE=23-67;
 CC NOE=Ref.1.
 CC -1- SIMILARITY: Belongs to the beta-defensin family.
 CC -----
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 CC -----
 CC DR EMBL; AY128668; AAM97293.1; -
 DR InterPro; IPR006080; Defensin_mammal.
 DR SMART; SM00048; DEFEN; 1.
 KW Antibiotic; Fungicide; Signal.
 FT SIGNAL 1 22 Potential.
 FT CHAIN 23 67 Beta-defensin 1.
 FT DISULFID 33 62 By similarity.
 FT DISULFID 40 55 By similarity.
 FT DISULFID 45 63 By similarity.
 SQ SEQUENCE 67 AA; 7676 MW; 30A611CDDC5BA8D CRC64;
 Query Match 84.6%; Score 302; DB 1; Length 67;
 Best Local Similarity 79.7%; Pred. No. 1.7e-27;
 Matches 51; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MRIHYLLFALLFLFVLPVPGHGIIINTLOKYYCVRVGRCAVLSCLPKREQIGKSTRGR 60
 DB 1 MRIHYLLFALLFLFVLPVPGHGIIINTLOKYYCVRVGRCAVLSCLPKREQIGKSTRGR 60
 QY 61 KCCR 64
 DB 61 KCCR 64
 Db 61 KCCR 64
 RESULT 5
 Q6SC68 PRELIMINARY; PRT; 67 AA.
 ID Q6SC68;
 AC Q6SC68;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Prepro-beta-defensin 3.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 OC NCBI_TaxID=96823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sang Y., Zhang G., Ross C.R., Blecha F.;
 RL Submitted (NOV-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY460575; AAR88759.1; -
 SQ SEQUENCE 67 AA; 7790 MW; 6BC28264846572AC CRC64;
 Query Match 83.5%; Score 298; DB 2; Length 67;
 Best Local Similarity 80.0%; Pred. No. 4.9e-27;
 Matches 52; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
 QY 1 MRIHYLLFALLFLFVLPVPGHGIIINTLOKYYCVRVGRCAVLSCLPKREQIGKSTRGR 60
 DB 1 MRIHYLLFALLFLFVLPVPGHGIIINTLOKYYCVRVGRCAVLSCLPKREQIGKSTRGR 60
 QY 61 KCCR 65
 DB 61 KCCR 65
 Db 61 KCCR 65
 RESULT 6
 AAR88759 PRELIMINARY; PRT; 67 AA.
 ID AAR88759;
 AC AAR88759;
 DT 02-MAR-2004 (TRENBLrel. 27, Created)

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DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Prepro-beta-defensin 3.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Sang Y., Zhang G., Ross C.R., Blecha F.;
RT "Characterization of porcine beta-defensin 3 and synergistic effect of
RT porcine beta-defensin 1, 2 and 3."
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY460575; AAR88759.1;
SQ SEQUENCE 67 AA; 7790 MW; 6BC28264846572AC CRC64;

Query Match 83.5%; Score 298; DB 2; Length 67;
Best Local Similarity 80.0%; Pred. No. 4.9e-27;
Matches 52; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 MRLHYLFLALFLFVLPVPGHGIINTLQKYCRVRGRCAYLSCLPKEQIGKSTGR 60
DB 1 MRLHYLFLALFLFVLPVPGHGIINTLQKYCRVRGRCAYLSCLPKEQIGKSTGR 60

QY 61 KCCRR 65
DB 61 KCCRR 65

RESULT 7
Q7TNV9 PRELIMINARY; PRT; 67 AA.
ID Q7TNV9;
AC 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Beta defensin 14.
GN Name=Defb14;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6;
RC Maxwell A.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Dorin J.R.;
RC STRAIN=C57BL/6;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ578468; CAB17665.2;
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:000613; P:response to pest/pathogen/parasite; IEA.
DR InterPro; IPR001855; Defensin_beta.
DR Pfam; PF00711; Defensin_beta.1.
SQ SEQUENCE 67 AA; 7718 MW; EEF0D93ADP17452 CRC64;

Query Match 71.7%; Score 256; DB 2; Length 67;
Best Local Similarity 67.7%; Pred. No. 3.9e-22;
Matches 44; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 MRLHYLFLALFLFVLPVPGHGIINTLQKYCRVRGRCAYLSCLPKEQIGKSTGR 60
DB 1 MRLHYLFLALFLFVLPVPGHGIINTLQKYCRVRGRCAYLSCLPKEQIGKSTGR 60

QY 61 KCCRR 65
DB 61 KCCRR 65

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RESULT 8
Q865P6 PRELIMINARY; PRT; 64 AA.
ID Q865P6;
AC 0865P6;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Beta-defensin-1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Sang Y., Davis E.G.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY170305; AA032801.1;
DR HSSP; P46170; IBBN.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:000613; P:response to pest/pathogen/parasite; IEA.
DR InterPro; IPR006080; Defensin_mammal.
DR SMART; SM00048; DEFSN; 1.
SQ SEQUENCE 64 AA; 6876 MW; 58C016282FBB4914 CRC64;

Query Match 40.1%; Score 143; DB 2; Length 64;
Best Local Similarity 46.2%; Pred. No. 5.8e-09;
Matches 30; Conservative 6; Mismatches 27; Indels 2; Gaps 1;

QY 1 MRLHYLFLALFLFVLPVPGHGIINTLQKYCRVRGRCAYLSCLPKEQIGKSTGR 60
DB 1 MRLHYLFLALFLFVLPVPGHGIINTLQKYCRVRGRCAYLSCLPKEQIGKSTGR 58

QY 61 KCCRR 65
DB 59 KCCRR 63

RESULT 9
ID02_PANTR STANDARD; PRT; 64 AA.
ID ID02_PANTR
AC 09JUL12;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-defensin 2 precursor (BD-2) (Defensin, beta 2).
GN Name=DEFB2; Synonyms=DEFB2, DEFB102;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Duts L.A., Langemann J.A.M., van der Straeten T., Verweene R.A.W.,
RA Pattansing S., Frost P.A., Hiemstra P.S., Thomas A.W., Nibbeling P.H.;
RT "Expression of beta-defensin-2 in chimpanzee (Pan troglodytes)."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Has antibacterial activity (potential).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: Belongs to the beta-defensin family. LAMP/TAP
CC subfamily.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; AF209855; AAF20154.1;
CC HSSP; O15263; IEA0
CC InterPro; IPR001855; Defensin_beta.

```

DR Pfam: PF00711; Defensin_beta; 1.
 KW Antibiotic; Signal.
 FT SIGNAL 1 23 Potential.
 FT CHAIN 24 64 Beta-defensin 2.
 FT DISULFID 31 60 By similarity.
 FT DISULFID 38 53 By similarity.
 FT DISULFID 43 61 By similarity.
 SQ SEQUENCE 64 AA; 7068 MW; B0D2454CE7ACDD13 CRC64;

Query Match 37.8%; Score 135; DB 1; Length 64;
 Best Local Similarity 42.4%; Pred No. 4.9e-08;
 Matches 28; Conservative 12; Mismatches 22; Indels 4; Gaps 2;

QY 1 MRHYLLFALLFLFVLPVPG-HGGIINTLQKYYCRVGRCAVLSCLPREQIGKCSRG 59
 DB 1 MRVLYLLFSPFLFLMPLPVGFGIGDPVT---CLKSGAICHVFPCPRRYKQIGTGLPG 57
 QY 60 KCCCR 65
 DB 58 TKCCCK 63

RESULT 10
 BD02_MACMU STANDARD; PRT; 64 AA.
 AC Q9BD59;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Beta-defensin 2 precursor (BD-2) (HBD-2) (Defensin, beta 2).
 GN Name=DEFB4; Synonyms=DEFB2;
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 NCBI_Taxid=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=11238224; DOI=10.1126/CDL.8.2.370-375.2001;
 RA Bala R., Yang C., Weiser D.U., Vogelmeier C., Weischi U., Wilson J.M.;
 RT "Rhesus monkey (Macaca mulatta) mucosal antimicrobial peptides are
 RT close homologues of human molecules.";
 RL Clin. Diagn. Lab. Immunol. 8:370-375(2001).
 CC -1- FUNCTION: Has antibacterial activity (Potential).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- SIMILARITY: Belongs to the beta-defensin family. LAMP/TAP
 subfamily.

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CC -----
 CC EMBL: AF288286; AAR26259.1; -
 DR HSSP; O15263; 1FD3.
 DR InterPro: IPR001855; Defensin_beta.
 DR InterPro: IPR006080; Defensin_mammal.
 DR Pfam: PF00711; Defensin_beta.1.
 DR SMART: SM00048; DEFSN; 1.
 DR Antibiatic; Signal.

KW Antibiotic; Signal.
 FT SIGNAL 1 23 Potential.
 FT CHAIN 24 64 Beta-defensin 2.
 FT DISULFID 31 60 By similarity.
 FT DISULFID 38 53 By similarity.
 FT DISULFID 43 61 By similarity.
 SQ SEQUENCE 64 AA; 7065 MW; BB24545CE7ACDDF CRC64;

Query Match 37.5%; Score 134; DB 1; Length 64;
 Best Local Similarity 42.4%; Pred. No. 6.5e-08;
 Matches 28; Conservative 12; Mismatches 22; Indels 4; Gaps 2;

QY 1 MRHYLLFALLFLFVLPVPG-HGGIINTLQKYYCRVGRCAVLSCLPREQIGKCSRG 59
 DB 1 MRVLYLLFSPFLFLMPLPVGFGIGDPVT---CLKSGAICHVFPCPRRYKQIGTGLPG 57
 QY 60 KCCCR 65
 DB 58 TKCCCK 63

RESULT 11
 BD02_HUMAN STANDARD; PRT; 64 AA.
 AC O15263;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Beta-defensin 2 precursor (BD-2) (HBD-2) (Defensin, beta 2) (Skin-
 DE antimicrobial peptide 1) (SAP1).
 GN Name=DEFB4; Synonyms=DEFB2, DEFB102;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin.
 RX MEDLINE=97345625; PubMed=9202117;
 RA Harder U., Bartels J.H., Christophers E., Schroeder J.-M.;
 RL "A peptide antibiotic from human skin".
 RL Nature 387:861-861(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=99051334; PubMed=9831658;
 RA Liu L., Wang L., Jia H.P., Zhao C., Heng H.H.Q., Schutte B.C.,
 RA McCray P.B. Jr., Ganz T.;
 RT "Structure and mapping of the human beta-defensin HBD-2 gene and its
 RT expression at sites of inflammation.";
 RL Gene 222:237-244(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20072673; PubMed=10603376;
 RA Diamond G., Kaiser V., Rhodes J., Russell J.P., Bevins C.L.;
 RT "Transcriptional regulation of beta-defensin gene expression in
 RT tracheal epithelial cells.";
 RL Infect. Immun. 68:113-119(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Harder U., Schroeder J.-M.;
 RT "Transcriptional regulation of the human beta-defensin-2 (HBD-2).";
 RT Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SYNTHESIS OF 24-64.
 RX MEDLINE=22007551; PubMed=12010514;
 RA Kluever E., Schulz A., Forssmann W.-G., Adermann K.;
 RT "Chemical synthesis of beta-defensins and DEAF-1/hepaticidin.";
 RL J. Pept. Res. 59:241-248(2002).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (1.35 ANGSTROMS).
 RX MEDLINE=20490730; PubMed=10906336; DOI=10.1074/jbc.M006098200;
 RA Hoover D.M., Rajashankar K.R., Blumenthal R., Puri A., Oppenheim J.J.,
 RA Chertov O., Lubkowski J.;
 RT "The structure of human beta-defensin-2 shows evidence of higher order
 RT oligomerization.";
 RL J. Biol. Chem. 275:32911-32918(2000).
 RN [7]
 RP STRUCTURE BY NMR OF 28-64.
 RX MEDLINE=21571984; PubMed=11714914;
 RA Bauer F., Schweimer K., Kluever E., Conejo-Garcia J.-R.,
 RA Forssmann W.-G., Rosch P., Adermann K., Sticht H.;
 RT "Structure determination of human and murine beta-defensins reveals
 RT structural conservation in the absence of significant sequence

RT similarity: 10:2470-2479 (2001).
 CC protein Sci. 10:2470-2479 (2001).
 CC -1- FUNCTION: Has antibacterial activity (Potential).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed in the skin and respiratory tract.
 CC -1- INDUCTION: By inflammation.
 CC -1- SIMILARITY: Belongs to the beta-defensin family. IAP/TAP subfamily.
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 CC
 CC EMBL: Z71389; CAA95992.1; -
 CC EMBL: AF040153; AAC33549.1; -
 CC EMBL: AF071216; AAC69554.1; -
 CC EMBL: AF000152; CAB65126.1; -
 CC PDB: 1E3Q; NMR; A=28-64.
 CC PDB: 1F03; X-ray; A/B/C/D=24-64.
 CC PDB: 1FD4; X-ray; A/B/C/D/E/F/G/H/I/J/K/L/M/N/O/P=24-64.
 CC PDB: 1FOO; NMR; A=24-64.
 CC Gene: HGNC:2767; DEFB4.
 CC MIM: 602215; -
 CC DR GO: GO:0006935; R:chemotaxis; TAS.
 CC DR GO: GO:0007186; R:G-protein coupled receptor protein signaln. .; TAS.
 CC DR GO: GO:0006955; R:immune response; TAS.
 CC DR GO: GO:0009613; R:response to pest/pathogen/parasite; TAS.
 CC DR InterPro: IPR001855; Defensin beta. 1.
 CC DR Pfam: PF00711; Defensin beta. 1.
 CC DR 3D-structure; Antibiotic; Signal.
 CC FT SIGNAL 1 23 Potential.
 CC FT CHAIN 24 64 Beta-defensin 2.
 CC FT DISULFID 31 60
 CC FT DISULFID 38 53
 CC FT DISULFID 43 61
 CC FT STRAND 25 26
 CC FT HELIX 28 33
 CC FT TURN 34 35
 CC FT STRAND 37 39
 CC FT TURN 45 46
 CC FT STRAND 48 52
 CC FT TURN 56 57
 CC FT STRAND 59 62
 CC SQ SEQUENCE 64 AA; 7038 MW; 05D6454CE7ACD10E CRC64;
 Query Match 37.3%; Score 133; DB 1; Length 64;
 Best Local Similarity 42.4%; Pred. No. 8.4e-08;
 Matches 28; Conservative 12; Mismatches 22; Indels 4; Gaps 2;
 QY 1 MRHYLPLALFLPLVPVPG-HGGIINTLQKYYCRVGRCAVLSCLPKEQIGKSTRG 59
 DB 1 MRVLYLPLFLPLVPVPG-HGGIINTLQKYYCRVGRCAVLSCLPKEQIGKSTRG 57
 QY 60 RKCCRR 65
 DB 58 TKCCCK 63
 RESULT 12
 AAH69285 PRELIMINARY; PRT; 64 AA.
 AC AAH69285;
 DT 01-JUN-2004 (TEMBLrel. 27, Created)
 DT 01-JUN-2004 (TEMBLrel. 27, Last sequence update)
 DE 01-JUN-2004 (TEMBLrel. 27, Last annotation update)
 GN Defensin, beta 4,,,
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxID=9606;
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusheva K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stacheron M., Soares M.B., Bonaldo R.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Tomshylski S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Keltman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman U.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood U., Schmutz U., Myers R.M., Butlerfield Y.S.,
 RA Krzywicki M.I., Skalska U., Smalius D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RX Strausberg R.L.
 RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC069285; AAH69285.1; -
 SQ SEQUENCE 64 AA; 7038 MW; 05D6454CE7ACD10E CRC64;
 Query Match 37.3%; Score 133; DB 2; Length 64;
 Best Local Similarity 42.4%; Pred. No. 8.4e-08;
 Matches 28; Conservative 12; Mismatches 22; Indels 4; Gaps 2;
 QY 1 MRHYLPLALFLPLVPVPG-HGGIINTLQKYYCRVGRCAVLSCLPKEQIGKSTRG 59
 DB 1 MRVLYLPLFLPLVPVPG-HGGIINTLQKYYCRVGRCAVLSCLPKEQIGKSTRG 57
 QY 60 RKCCRR 65
 DB 58 TKCCCK 63
 RESULT 13
 BD03 MOUSE
 ID BD03 MOUSE STANDARD; PRT; 63 AA.
 AC G9MTL0;
 DT 16-OCT-2001 (rel. 40, Created)
 DT 05-OCT-2004 (rel. 44, Last sequence update)
 DE Beta-defensin 3 precursor (BD-3) (MBD-3).
 GN Name=Defb3; Synonyms=Bd3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, INDUCTION, AND TISSUE SPECIFICITY.
 RC STRAIN=C57BL/6; TISSUE=Lung;
 RX MEDLINE=9307216; PubMed=10377137;
 RA Bales R., Wang X., Meegalla R.L., Wattler S., Weiner D.J., Nehls M.C.,
 RA Wilson J.M.,
 RT "Mouse beta-defensin 3 is an inducible antimicrobial peptide expressed
 RT in the epithelia of multiple organs."
 RL Infect. Immun. 67:3542-3547 (1999).
 RN [2]
 RP TISSUE SPECIFICITY.
 RC STRAIN=C57BL/6, 129/SvJ and FVB; TISSUE=Lung;
 RX MEDLINE=20517883; PubMed=10922379;

RA Jia H.P., Wock S.A., Schutte B.C., Lee S.K., Vivado A., Tack B.F.,
 RA Bevins C.L., McCreary P.B. Jr.;
 RT "A novel murine beta-defensin expressed in tongue, esophagus, and
 RT trachea.";
 RL J. Biol. Chem. 275:33314-33320(2000).
 CC -1- FUNCTION: Antimicrobial activity against Gram-negative bacteria
 CC E.coli and P.aeruginosa.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Highest expression in salivary glands,
 CC epididymis, ovary and pancreas and to a lesser extent in lung,
 CC liver and brain. Low or no expression in skeletal muscle and
 CC tongue.
 CC -1- INDUCTION: By bacterial infection.
 CC -1- SIMILARITY: Belongs to the beta-defensin family. LAP/TAP
 CC subfamily.
 CC -----
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 CC -----
 CC EMBL: AF093245; AAD29573.1; -;
 CC EMBL: AF092929; AAD29572.1; -;
 CC HSSP: O15263; 1E4Q.
 CC MGD: MGI:1351612; Defb3.
 CC InterPro: IPR001855; Defensin_beta.
 CC InterPro: IPR006080; Defensin_mammal.
 CC Pfam: PF00711; Defensin_beta; 1.
 CC SMART: SM00048; DEFSN; 1.
 CC Antibiotic: cleavage on pair of basic residues; Signal.
 CC SIGNAL 1 20 Potential.
 CC PROPEP 21 22
 CC CHAIN 23 63 Beta-defensin 3.
 CC DISULFID 31 59 By similarity.
 CC DISULFID 38 52 By similarity.
 CC DISULFID 42 60 By similarity.
 CC SEQUENCE 63 AA; 7126 MW; 9D59BC8AD16A330 CRC64;
 SQ
 Query Match 32.6%; Score 116.5; DB 1; Length 63;
 Best Local Similarity 43.1%; Pred. No. 7e-06;
 Matches 28; Conservative 4; Mismatches 30; Indels 3; Gaps 2;
 QY 1 MRLHYLLFLLFLFVPVPGHGIINTLOKYYCRVGRGCAVLSCLPREEOIGKSTRGR 60
 DB 1 MRLHYLLFLLFLFVLVLSPPAASFKIN--NPVSCLRKGRG--MRLGINTROIIGSCVPL 57
 QY 61 KCCR 65
 DB 58 KCCR 62
 RESULT 14
 EAP BOVIN STANDARD; PRT; 64 AA.
 ID EAP BOVIN
 AC 002775;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Enteric beta-defensin precursor.
 GN Name=EBD;
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovinae; Bos.
 CC NCBI_TaxID=9913;
 CC (1)
 RN SEQUENCE FROM N.A.
 RP MEDLINE=98147718; PubMed=9488394;
 RA Tarter A.P., Clark D.P., Diamond G., Russell J.P.,
 RA Erdjument-Bronage H., Tempst P., Cohen K.S., Jones D.E., Sweeney R.W.,

RA Wines M., Hwang S., Bevins C.L.;
 RT "Enteric beta-defensin: molecular cloning and characterization of a
 RT gene with inducible intestinal epithelial cell expression associated
 RT with Cryptosporidium parvum infection.";
 RL Infect. Immun. 66:1045-1056(1998).
 CC (2)
 CC SEQUENCE FROM N.A.
 CC MEDLINE=96014297; PubMed=8589529;
 RA Gallagher D.S. Jr.; Ryan A.M., Diamond G., Bevins C.L., Womack J.E.;
 RT "Somatic cell mapping of beta-defensin genes to cattle syntenic group
 RT u25 and fluorescence in situ localization to chromosome 27.";
 RL Mamm. Genome 6:554-556(1995).
 CC -1- FUNCTION: Has antibacterial activity (Potential).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Inducibly expressed in enteric epithelial
 CC cells.
 CC -1- SIMILARITY: Belongs to the beta-defensin family. LAP/TAP
 CC subfamily.
 CC -----
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 CC -----
 CC EMBL: AF000362; AAC48805.1; -;
 CC EMBL: AF016539; AAC48804.1; -;
 CC HSSP: P46170; 1BNB.
 CC InterPro: IPR001855; Defensin_beta.
 CC InterPro: IPR006080; Defensin_mammal.
 CC Pfam: PF00711; Defensin_beta; 1.
 CC SMART: SM00048; DEFSN; 1.
 CC Antibiotic: Signal.
 CC SIGNAL 1 26 By similarity.
 CC CHAIN 27 64 Enteric beta-defensin.
 CC DISULFID 31 60 By similarity.
 CC DISULFID 38 53 By similarity.
 CC DISULFID 43 61 By similarity.
 CC SEQUENCE 64 AA; 7126 MW; 7B642ABEF7A6068 CRC64;
 SQ
 Query Match 32.5%; Score 116; DB 1; Length 64;
 Best Local Similarity 44.6%; Pred. No. 8.1e-06;
 Matches 29; Conservative 4; Mismatches 28; Indels 4; Gaps 2;
 QY 1 MRLHYLLFLLFLFVPVPGH--GGIINTLOKYYCRVGRGCAVLSCLPREEOIGKSTRG 59
 DB 1 MRLHYLLFLLFLFVLVLSAGSGFTQGISNPDS---CRLNIGICVPIRCGRLRGIGTCFTPS 57
 QY 60 KCCR 64
 DB 58 KCCR 62
 RESULT 15
 Q71UAS PRELIMINARY; PRT; 60 AA.
 ID Q71UAS
 AC Q71UAS;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Neutrophil beta-defensin 12 (Fragment).
 GN Name=NB012;
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovinae; Bos.
 CC NCBI_TaxID=9913;
 CC (1)
 RN SEQUENCE FROM N.A.
 RP MEDLINE=99403068; PubMed=10473579;
 RA Yount N.Y., Yuan J., Tarter A., Castro T., Diamond G., Tran P.A.,

RA Levy J.N., McCullough C., Cullor J.S., Bevins C.L., Selsted M.E.;
RT "Cloning and expression of bovine neutrophil beta-defensins.
RT Biochemical profile during neutrophilic maturation and localization
RT of mature peptide to novel cytoplasmic dense granules.";
RL J. Biol. Chem. 274:26249-26258(1999).
DR EMBL; AF105370; AAD43032.1; JOINED.
DR EMBL; AF105371; AAD43032.1; -.
DR InterPro; IPR001855; Defensin_beta.
DR InterPro; IPR006080; Defensin_mammal.
DR Pfam; PF00711; Defensin_beta; 1.
DR SMART; SM00046; DEFSN; 1.
FT NON_TER 60 60
SQ SEQUENCE 60 AA; 6464 MW; 3866879EACF6D6 CRC64;
Query Match 32.2%; Score 115; DB 2; Length 60;
Best Local Similarity 42.2%; Pred. 1e-05;
Matches 27; Conservative 5; Mismatches 26; Indels 6; Gaps 1;
QY 1 MRLHLLFALLFLVPGHGGINTLQKYCRVGRCAVLSCLPKEQIGKSTGR 60
DB 1 MRLHLLFALLFLVLAASGISGPLS-----CGRNGVCIPRCFVPMRQIGTCGRPV 54
QY 61 KCCR 64
DB 55 KCCR 58

Search completed: October 13, 2004, 14:50:38
Job time : 200 secs

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OK protein - protein search, using sw model

Run on: October 13, 2004, 14:42:12 ; Search time 39 Seconds
(without alignments)
160.361 Million cell updates/sec

Title: US-10-272-121-2

Perfect score: 357
Sequence: 1 MRLHYLFLALLFLVLPVPG.....LPKEQIGKSTRKRCRR 65

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	108	30.3	64	2	A56128	lingual antimicrob
2	108	30.3	65	2	A35947	crocamine 1 precu
3	108	30.3	65	2	C35947	crocamine 3 precu
4	108	29.7	64	2	A47438	airway epithelial
5	103	28.9	65	2	JC5324	myotoxin a precu
6	89	24.9	42	2	F45495	beta-defensin-6 -
7	83	23.2	64	2	B35947	crocamine 2 precu
8	75	21.0	38	2	B47753	beta-defensin-11 -
9	71	19.9	42	2	C45495	beta-defensin-3 -
10	69.5	19.5	45	1	A37909	myotoxin - easter
11	69.5	19.5	95	1	WTRBM1	macrophage antibi
12	69	19.3	40	2	I45495	beta-defensin-9 -
13	69	19.3	40	2	I45495	beta-defensin-9 -
14	68	19.0	42	2	D47753	beta-defensin-13 -
15	66.5	18.6	43	1	CXRSC8	toxic peptide C -
16	65.5	18.3	95	1	CXRSC8	crocamine - tropic
17	65.5	18.3	95	1	WTRBM2	crocamine CS-4 prec
18	63.5	17.8	51	1	D35947	crocamine 4 precu
19	62.5	17.5	42	1	MXRSMV	myotoxin a 6 - pra
20	61	17.1	122	2	JC2648	high sulfur protei
21	61	17.1	122	2	JC2648	hypothetical prote
22	61	17.1	122	2	JC2648	hypothetical prote
23	61	17.1	122	2	JC2648	hypothetical prote
24	60.5	16.9	40	2	C39560	myotoxin a 5 - pra
25	60	16.8	32	2	E59076	defensin alpha-5 -
26	60	16.8	32	2	E59076	defensin alpha-4 -
27	60	16.8	33	2	D59076	defensin alpha-7 -
28	60	16.8	33	2	D59076	defensin alpha-6 -
29	60	16.8	855	2	T05981	hypothetical prote

30	59.5	16.7	260	2	AD2461	hypothetical prote
31	59.5	16.7	454	2	B82412	probable magnesium
32	59.5	16.7	1184	2	T03484	carilage intermed
33	59.5	16.7	40	2	E45495	beta-defensin-5 -
34	59	16.5	177	2	S57346	high-sulfur kerat
35	59	16.5	263	2	S57346	interleukin 15 rec
36	58.5	16.4	43	2	A23089	myotoxin I - midge
37	58.5	16.4	45	2	S12909	myotoxin - western
38	58.5	16.4	88	2	H69475	hypothetical prote
39	58.5	16.4	112	2	A46717	collipase precursor
40	58.5	16.4	359	2	A96816	P920.25 (imported
41	58	16.2	34	2	C49195	coricostatic pept
42	58	16.2	152	2	I47109	high-sulfur wool m
43	58	16.2	152	2	I47112	high-sulfur wool m
44	58	16.2	162	2	I47107	high-sulfur wool m
45	58	16.2	172	1	KRSHHA	keratin high-sulfu

ALIGNMENTS

RESULT 1
A56128
lingual antimicrobial peptide precursor - bovine
C/Species: Bos primigenius taurus (cattle)
C/Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
C/Accession: A56128; B56128
R/Schönwetter, B.S.; Stolzenberg, E.D.; Zasloff, M.A.
Science 267, 1645-1648, 1995
A/Title: Epithelial antibiotics induced at sites of inflammation.
A/Reference number: A56128; PMID:95192714; PMID:7886453
A/Accession: A56128
A/Molecule type: mRNA
A/Residues: 1-64 <SCH>
A/Cross-references: UNIPROT:Q28880; GB:S76279; NID:g894208; PIDN:AMB33727.1; PID:g89420
A/Accession: B56128
A/Molecule type: protein
A/Residues: 23-64 <SC2>
C/Keywords: antibacterial; antifungal
F/1-20/Domain: signal sequence #status predicted <SIG>
F/23-64/Product: lingual antimicrobial peptide #status experimental <MAT>

Query Match 30.3%; Score 108; DB 2; Length 64;

Best Local Similarity 41.5%; Pred. No. 1.7e-05;

Matches 27; Conservative 3; Mismatches 33; Indels 2; Gaps 1;

QY 1 MRLHYLFLALLFLVLPVPGHGIINTLOKYYRVRGRCVAVSCLEKEQIGKSTRGR 60
DB 1 MRLHYLFLALLFLVLPVPGHGIINTLOKYYRVRGRCVAVSCLEKEQIGKSTRGR 60

QY 61 KCCR 65
DB 59 KCCR 63

RESULT 2

A35947
crocamine 1 precursor - tropical rattlesnake
C/Species: Crocalus durissus terrificus (tropical rattlesnake, cascade)
C/Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 09-Jul-2004
C/Accession: A35947
R/Smith, L.A.; Schmidt, J.J.
Toxicol 28, 575-585, 1990
A/Title: Cloning and nucleotide sequences of crocamine genes.
A/Reference number: A35947; PMID:90357261; PMID:2389256
A/Accession: A35947
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-65 <SM1>
A/Cross-references: UNIPROT:P24331
C/Superfamily: crocamine

Query Match 30.3%; Score 108; DB 2; Length 65;

Best Local Similarity 39.1%; Pred. No. 1.8e-05;
Matches 27; Conservative 9; Mismatches 21; Indels 12; Gaps 5;
Qy 1 MRHVLFPALFLFPLVPVPGHGIINTLQKYCYVRGRCAYLS--CLPKKEQIGK--CS 56
Db 1 MKLILFLFALFLFPLFPLFSEFG-----NAYKR--CHIKGHCPRKXKICIPSSDGRKMDCP 53
Qy 57 TRGRKCCR 65
Db 54 WR-RKCCR 61

RESULT 3
C35947
crostamine 3 precursor - tropical rattlesnake
C/Species: Crocalus durissus terrificus (tropical rattlesnake, cascabel)
C/Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 09-Jul-2004
C/Accession: C35947
R/Smith, L.A.; Schmidt, J.J.
Toxicon 28, 575-585, 1990
A/Title: Cloning and nucleotide sequences of crostamine genes.
A/Reference number: A35947; MUID:90557261; PMID:2389256
A/Accession: C35947
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-65 <SMI>
A/Cross-references: UNIPROT:P24333
C/Superfamily: crostamine

Query Match 30.3%; Score 108; DB 2; Length 65;
Best Local Similarity 39.1%; Pred. No. 1.8e-05;
Matches 27; Conservative 9; Mismatches 21; Indels 12; Gaps 5;

Qy 1 MRHVLFPALFLFPLVPVPGHGIINTLQKYCYVRGRCAYLS--CLPKKEQIGK--CS 56
Db 1 MKLILFLFALFLFPLFPLFSEFG-----NAYKR--CHIKGHCPRKXKICIPSSDGRKMDCP 53

Qy 57 TRGRKCCR 65
Db 54 WR-RKCCR 61

RESULT 4
A47438
airway epithelial antimicrobial peptide TAP precursor - bovine

N/Alternate names: antimicrobial peptide, tracheal
C/Species: Bos primigenius taurus (cattle)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: A47438; A39397

R/Diamond, G.; Jones, D.E.; Bevins, C.L.
Proc. Natl. Acad. Sci. U.S.A. 90, 4596-4600, 1993

A/Title: Airway epithelial cells are the site of expression of a mammalian antimicrobial
A/Reference number: A47438; MUID:93281626; PMID:8506305
A/Accession: A47438

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-64 <DIA>

A/Cross-references: UNIPROT:P25068; GB:U13373; NID:G289395; PIDN:AA72363.1; PID:G289396
R/Diamond, G.; Zaslaf, M.; Eck, H.; Brasseur, M.; Maloy, W.L.; Bevins, C.L.
Proc. Natl. Acad. Sci. U.S.A. 88, 3952-3956, 1991

A/Title: Tracheal antimicrobial peptide, a cysteine-rich peptide from mammalian tracheal
A/Reference number: A39397; MUID:91219490; PMID:2023343
A/Accession: A39397

A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-64 <DIA>

A/Cross-references: GB:M63023; NID:G2226433; PIDN:AA61757.1; PID:G163740
C/Genetics: 19/2

F/1-26/Domain: signal sequence #status predicted <SIG>
F/27-66/Product: airway epithelial antimicrobial peptide TAP #status predicted <MAT>

Query Match 29.7%; Score 106; DB 2; Length 64;

Best Local Similarity 40.9%; Pred. No. 2.9e-05;
Matches 27; Conservative 7; Mismatches 28; Indels 4; Gaps 2;
Qy 1 MRHVLFPALFLFPLVPVPGHGIINTLQKYCYVRGRCAYLSCLPKKEQIGKSTRG 59
Db 1 MRHVLFPALFLFPLVLSAMSGTQGVNPS---CVRNKIGICVPIRCPGSMKQIGTCVRA 57
Qy 60 RKCCR 65
Db 58 VKCCR 63

RESULT 5
JC5324
myotoxin a precursor - prairie rattlesnake
C/Species: Crocalus viridis viridis (prairie rattlesnake)
C/Date: 15-May-1997 #sequence_revision 18-Jul-1997 #text_change 02-Jul-1998
C/Accession: JC5324
R/Norris, U.W.; Fry, R.M.; Tu, A.T.
Biochem. Biophys. Res. Commun. 230, 607-610, 1997
A/Title: The nucleotide sequence of the translated and untranslated regions of a cDNA f
A/Reference number: JC5324; MUID:97167753; PMID:9015371
A/Accession: JC5324
A/Molecule type: mRNA
A/Residues: 1-65 <NOR>
A/Experimental source: venom
A/Note: The authors translated the codon CAG for residue 27 as His and CTT for residue
C/Comment: This protein inhibits Ca2+ uptake into the sarcoplasmic reticulum by binding
C/Superfamily: crostamine
F/1-22/Domain: signal sequence #status predicted <SIG>
F/23-64/Product: myotoxin a #status predicted <MAT>

Query Match 28.9%; Score 103; DB 2; Length 65;
Best Local Similarity 36.8%; Pred. No. 6.6e-05;
Matches 25; Conservative 11; Mismatches 22; Indels 10; Gaps 4;

Qy 1 MRHVLFPALFLFPLVPVPGHGIINTLQKYCYVRGRCAYLS--CLPKKEQIGKSTRG 58
Db 1 MKLILFLFALFLFPLFPLFSEFG-----NAYKO--CQKKGHCPRKXKICIPSSDLGMDCR 53

Qy 59 GR-KCCR 65
Db 54 WKMKCCR 61

RESULT 6

F45495
beta-defensin-6 - bovine

N/Alternate names: peptide BND-6
C/Species: Bos primigenius taurus (cattle)
C/Date: 24-Feb-1994 #sequence_revision 22-Apr-1995 #text_change 09-Jul-2004
C/Accession: F45495

R/Selsted, M.E.; Tang, Y.O.; Morris, W.L.; McGuire, P.A.; Novorny, M.J.; Smith, W.; Hen
U. Biol. Chem. 268, 6641-6648, 1993
A/Title: Purification, primary structures, and antibacterial activities of beta-defensi
A/Reference number: A45495; MUID:93203264; PMID:8454635
A/Accession: F45495

A/Molecule type: protein
A/Residues: 1-42 <SE>

A/Cross-references: UNIPROT:P46164

A/Note: sequence modified after extraction from NCBI backbone
C/Keywords: antibacterial, disulfide bond, pyroglutamic acid
F/1-42/Product: beta-defensin-6 #status experimental <MAT>

F/1-Modified site: pyroglutamic acid (Gln) #status experimental
F/9-38,16-31,21-39/Disulfide bonds: #status predicted

Query Match 24.9%; Score 89; DB 2; Length 42;
Best Local Similarity 48.5%; Pred. No. 0.0019;
Matches 16; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Qy 33 CRVGRCAVLSCLPKKEQIGKSTRGRKCCR 65
Db 9 CRVGRCAVLSCLPKKEQIGKSTRGRKCCR 41

RESULT 7

crotamine 2precursor - tropical rattlesnake (fragment)
 C:Species: Crotalus durissus terrificus (tropical rattlesnake, cascabel)
 C:Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #next_change 09-Jul-2004
 C:Accession: B35947
 R:Smith, L.A.; Schmidt, J.J.
 Toxicol 28, 575-585, 1990
 A:Title: Cloning and nucleotide sequences of crotamine genes.
 A:Accession number: A35947; PMID:190357261; PMID:2189256
 A:Accession: B35947
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-64 <SMT>
 A:Cross-references: UNIPROT:P24332
 C:Superfamily: crotamine

Query Match:	23.2%	Score 83;	DB 2;	Length 64;
Best Local Similarity:	35.3%;	Pred. No.	0.013;	
Matches 24;	Conservative	9;	Mismatches 23;	Indels 12;
				Gaps 5;

Oy

2 RIHYLLFALLPFVLVPVPGGGIINTLQRYCYRVRGGRCAVL--CLPKPEQIGK--CST 57
::|||::|::|:
Db

1 KIYLTLFAFLFAFLSEPG----NAYKR--CHIKGGHCPEKEKICIPSSDFGMDCPW 53

```
QY      58 RGRKCCRR 65
      59 | | | : :
Db      54 R-RKSLKK 60
```

RESULT 8
B47753

```

N|Alternate names: peptide BMBD-11
C|Species: Bos primigenius taurus (cattle)
C|Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C|Accession: B47753
R|Separated, M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Heng
J|Biol. Chem. 268, 6641-6648, 1993
A|Title: Purification, primary structures, and antibacterial activities of beta-defensin
A|Reference number: A45495; MUID:93203264; PMID:8454635
A|Accession: B47753
A|Molecule type: protein
A|Residues: 1-38 <SEL>
A|Cross-references: UNIPROT:P46169
A|Note: sequence extracted from NCBI backbone (NCBI:P127961)
C|Keywords: antibacterial, disulfide bond
F|1-18/Product: beta-defensin-11 #stratus experimental <MAL>
F|5-34,12-27,17-35/Disulfide bonds: #stratus predicted

```

Query Match	21.0 %;	Score 75;	DB 2;	Length 38;
Best Local Similarity	46.9 %;	Pred No. 0.072;		
Matches 15;	Conservative	1;	Mismatches 16;	Indels 0;
			Gaps	0

QY 33 CRVRGRCAYLSCLPKEDQIGKSTGRKKCR 64
||| : |||||
Db 5 CRRNGVCIPRCGPMRQIGTCFGRPVKCCR 36

RESULT 5
C45495

beta-defensin-3 - bovine
N:Alternate names: peptide BNBD-3
N:Contains: beta-defensin-2
C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Feb-1994 #sequence revision 22-Apr-1995 #text_change 09-Jul-2004
C:Accession: C45495; Y45495
R:Selected: M.E. Tang, B.O. Morris, W.L. McGuire, P.A. Novotny, M.J. Smith, W. Hens
J Biol Chem 268 6641-6648, 1993
A:Title: Purification, primary structures, and antibacterial activities of beta-defensin
A:Reference number: A45495; M01D:93203264; PMID:945635

A;Accession: C45495
A;Molecule type: protein
A;Database: 1-3

A:Cross-references: UNIPROT:P46160
A:Note: sequence modified after extraction from NCBI backbone
A:Accession: B45495
A:Molecule type: protein
A:Mass: 343 kDa

Query Match	19.94;	Score 71;	DB 2;	Length 42;
Best Local Similarity	40.64;	Pred. No. 0.22;		
Matches 13;	Conservative 3;	Mismatches 16;	Indels 0;	Gaps 0;

```
QY      33 CRVRGRCVAVLSCLPKKEQIGKSTGRKKCCR   64
          ||| : | : ||| ||||
Db       9 CRINEGCVPIRCPPGRTRQIGTCFPRIKCCR   40
```

RESULT 10

myotoxin - eastern diamondback rattlesnake
M:Species: Crotalus adamanteus (eastern diamondback rattlesnake)
C:Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #ext_change 09-Jul-2004
C:Accession: A37909
R:Samejima, Y.; Koki, Y.; Mabe, D.
Toxicol 29, 461-468, 1991
A:Title: Amino acid sequence of a myotoxin from venom of the eastern diamondback rattlesnake
A:Reference number: A37909; MUID:9130359; PMID:166251
A:Accession: A37909
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-45 <SAM>
A:Cross-references: UNIPROT:P24330
C:Superfamily: crotaline
C:Keywords: myotoxin

Query Match	19.5%	Score	69.5	DB	2	Length	45
Best Local Similarity	38.9%	Pred. No.	0.35				
Matches	14	Conservative	4	Mismatches	15	Indels	3
						Gaps	2

Oy 33 CRVRGRC--AVLSCLPKEDIGKCSIRGR-KCCRR 65
| : || | | | |
Db 4 CHKGSGCFPXTVICTLPPSSDFGMDCRWRWCKCK 39

RESULT 11

macrophage antibiotic peptide MCP-1 - rabbit
 M.ALternate names: antidiuretic/ototropin, corticostatic peptide CS-3; defensin
 C1Species: *Oryctolagus cuniculus* (domestic rabbit)
 C.Date: 28-Aug-1985 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
 C.Accession: A45811, J01447, X22568, B43195
 R.Ganz, T.; Kayner, C.R.; Valdez, E.V.; Timpl, A.; Talmadge, K.; Fuller, F.
 J. Immunol. 143, 1358-1365, 1989
 A.Title: The structure of the rabbit macrophage defensin genes and their organ-specific
 A.Reference number: A45811, MUID:85309825, PMID:12743983

A:status: preliminary
A:molecule type: DNA
A:Residues: 1-95 <GAP>
A:Cross-references: UNIPROT:P01376; GB:M28072; NID:G165473; PIDN:AAA31388.1; PID:G165474
R:Related, M.E.; Brown, D.M.; Delange, R.J.; Lehrer, R.I.
J. Biol. Chem. 258: 14485-14489, 1983
A:title: Primary structures of MCP-1 and MCP-2, natural peptide antibiotics of rabbit leukocytes
A:Reference number: A01647; MUID:84061901; PMID:663457
A:Accession: A01647
A:molecule type: protein

A:Residues: 63-95 <SEL>
 R:Selected: M.E.; Brown, D.M.; Delange, R.J.; Harwig, S.S.L.; Lehrer, R.I.
 J. Biol. Chem. 260, 4579-4584, 1985
 C:Species: Bos primigenius taurus (cattle)
 A:Title: Primary structures of six antimicrobial peptides of rabbit peritoneal neutrophils
 A:Reference number: A22565; MUID:85182561; PMID:3988726
 A:Accession: A22569
 A:Molecule type: protein
 A:Residues: 63-95 <SEL>
 A:Experimental source: peritoneal neutrophils
 R:Zhu, O.; Solomon, S.
 Endocrinology 130, 1413-1423, 1992
 A:Title: Isolation and mode of action of rabbit corticostatic (antidiureticocortropin)
 A:Reference number: A49195; MUID:92164536; PMID:1311240
 A:Accession: B49195
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 63-95 <ZHU>
 A:Note: sequence extracted from NCBI backbone (NCBI:P46166)
 C:Comment: This peptide is active against some fungi and gram-positive bacteria in vitro
 C:Superfamily: mammalian defensin
 C:Keywords: antibacterial
 F:5-93,67-82,72-92/Disulfide bonds: #status predicted

Query Match 19.5%; Score 69.5; DB 1; Length 95;
 Best Local Similarity 48.3%; Pred. No. 0.65;
 Matches 14; Conservative 2; Mismatches 10; Indels 3; Gaps 1;

QY 40 CAVLSCLPKKEQIGKSTGR--KCCR 65
 DB 67 CRRALCLPRERRAGFCRRGRHPLCCRR 95

RESULT 12
 G45495
 beta-defensin-7 - bovine
 N:Alternate names: peptide BND-7
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 24-Feb-1994 #sequence_revision 22-Apr-1995 #text_change 09-Jul-2004
 C:Accession: G45495
 R:Selected: M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hen
 J. Biol. Chem. 268, 6641-6648, 1993
 A:Title: Purification, primary structures, and antibacterial activities of beta-defensin
 A:Reference number: A45495; MUID:93203264; PMID:8454635
 A:Accession: G45495
 A:Molecule type: protein
 A:Residues: 1-40 <SEL>
 A:Cross-references: UNIPROT:P46165
 A:Note: sequence modified after extraction from NCBI backbone
 C:Keywords: antibacterial, disulfide bond, pyroglutamic acid
 F:1-40/Product: beta-defensin-7 #status experimental <MA1>
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:9-38,16-31,21-39/Disulfide bonds: #status predicted

Query Match 19.3%; Score 69; DB 2; Length 40;
 Best Local Similarity 40.6%; Pred. No. 0.37;
 Matches 13; Conservative 2; Mismatches 17; Indels 0; Gaps 0;

QY 33 CRVGRCAVLSCLPKKEQIGKSTGRKCCR 64
 DB 9 CRNRGCVPIRCPGHRROIGTGLGPRKCCR 40

RESULT 13
 I45495
 beta-defensin-9 - bovine
 N:Alternate names: peptide BND-9
 N:Contains: beta-defensin-8
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 24-Feb-1994 #sequence_revision 22-Apr-1995 #text_change 09-Jul-2004
 C:Accession: I45495; H45495
 R:Selected: M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hen
 J. Biol. Chem. 268, 6641-6648, 1993
 A:Title: Purification, primary structures, and antibacterial activities of beta-defensin

A:Reference number: A45495; MUID:93203264; PMID:8454635
 A:Accession: I45495
 A:Molecule type: protein
 A:Residues: 1-40 <SEL>
 A:Cross-references: UNIPROT:P46166
 A:Note: sequence modified after extraction from NCBI backbone
 A:Accession: H45495
 A:Molecule type: protein
 A:Residues: 3-40 <SEL>
 A:Note: sequence extracted from NCBI backbone (NCBI:P127958)
 C:Keywords: pyroglutamic acid
 F:1-40/Product: beta-defensin-9 #status experimental <MA1>
 F:3-40/Product: beta-defensin-8 #status experimental <MA2>
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:9-38,16-31,21-39/Disulfide bonds: #status predicted

Query Match 19.3%; Score 69; DB 2; Length 40;
 Best Local Similarity 40.6%; Pred. No. 0.37;
 Matches 13; Conservative 2; Mismatches 17; Indels 0; Gaps 0;

QY 33 CRVGRCAVLSCLPKKEQIGKSTGRKCCR 64
 DB 9 CRNRGCVPIRCPGHRROIGTGLGPRKCCR 40

RESULT 14
 D47753
 beta-defensin-13 - bovine
 N:Alternate names: peptide BND-13
 N:Contains: beta-defensin-12
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C:Accession: D47753; C47753
 R:Selected: M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hen
 J. Biol. Chem. 268, 6641-6648, 1993
 A:Title: Purification, primary structures, and antibacterial activities of beta-defensin
 A:Reference number: A45495; MUID:93203264; PMID:8454635
 A:Accession: D47753
 A:Molecule type: protein
 A:Residues: 1-42 <SEL>
 A:Cross-references: UNIPROT:P46171
 A:Note: sequence extracted from NCBI backbone (NCBI:P127963)
 A:Accession: C47753
 A:Molecule type: protein
 A:Residues: 5-42 <SEL>
 A:Note: sequence extracted from NCBI backbone (NCBI:P127962)
 C:Keywords: disulfide bond
 F:1-42/Product: beta-defensin-13 #status experimental <MA1>
 F:5-42/Product: beta-defensin-12 #status experimental <MA2>
 F:9-38,16-31,21-39/Disulfide bonds: #status experimental

Query Match 19.0%; Score 68; DB 2; Length 42;
 Best Local Similarity 43.8%; Pred. No. 0.5;
 Matches 14; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

QY 33 CRVGRCAVLSCLPKKEQIGKSTGRKCCR 64
 DB 9 CGRNGVCIPIRCPVPRROIGTGRVPRKCCR 40

RESULT 15
 CRRSCH
 toxic peptide C - southern Pacific rattlesnake
 C:Species: Crotalus viridis helleri (southern Pacific rattlesnake)
 C:Date: 31-May-1979 #sequence_revision 08-Oct-1981 #text_change 09-Jul-2004
 C:Accession: A01737
 R:Maeda, N.; Tamiya, N.; Pattachiraman, T.R.; Russell, F.E.
 Toxicon 16, 431-441, 1978
 A:Title: Some chemical properties of the venom of the rattlesnake, Crotalus viridis hel
 A:Reference number: A01737; MUID:79015339; PMID:694946
 A:Accession: A01737
 A:Molecule type: protein
 A:Residues: 1-43 <MA>

A:Cross-references: UNIPROT:P01477

C:Superfamily: crotoxin

C:Keywords: myotoxin; venom

F:4-36,11-30,18-37/Disulfide bonds: #status predicted

Query Match 18.6%; Score 66.5; DB 1; Length 43;

Best Local Similarity 36.1%; Pred. No. 0.76;

Matches 13; Conservative 5; Mismatches 15; Indels 3; Gaps 2;

Oy 33 CRVNGRC--AVLSCLPKKEQIGKSTRGR-KCGR 65

Db 4 CHKKGHCFFKTVICLPSSDFGRKDCRKNKCCRK 39

Search completed: October 13, 2004, 14:51:17
Job time : 40 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compen Ltd.

OM protein - protein search, using sw model

Run on: October 13, 2004, 14:44:44 ; Search time 131 Seconds
(without alignments)
160.110 Million cell updates/sec

Title: US-10-272-121-2

Perfect score: 357
Sequence: 1 MHIHLFLLFLFVLPVPG.....LPKRGQIGKSTRGKRCRR 65

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1356558 seqs, 322682953 residues

Total number of hits satisfying chosen parameters: 1356558

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: Published Applications_AA.*
2: /cgn2_6/prodata/1/pubppa/US07_PUBCOMB.pep.*
3: /cgn2_6/prodata/1/pubppa/PCT_NEW_PUB.pep.*
4: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB.pep.*
5: /cgn2_6/prodata/1/pubppa/US06_PUBCOMB.pep.*
6: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB.pep.*
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18: /cgn2_6/prodata/1/pubppa/US60_NEW_PUB.pep.*
19: /cgn2_6/prodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	357	100.0	65	14 US-10-091-166B-2	Sequence 2, Appl1
2	357	100.0	65	14 US-10-272-121-2	Sequence 2, Appl1
3	357	100.0	65	14 US-10-409-366-2	Sequence 2, Appl1
4	357	100.0	65	14 US-10-409-532-2	Sequence 2, Appl1
5	357	100.0	67	9 US-09-917-340-52	Sequence 52, Appl1
6	357	100.0	67	9 US-09-917-340-72	Sequence 72, Appl1
7	357	100.0	67	9 US-09-872-852-2	Sequence 2, Appl1
8	357	100.0	67	14 US-10-091-166B-10	Sequence 10, Appl1
9	357	100.0	67	14 US-10-272-121-10	Sequence 10, Appl1
10	357	100.0	67	14 US-10-409-366-10	Sequence 10, Appl1
11	357	100.0	67	14 US-10-409-532-10	Sequence 10, Appl1
12	240	67.2	45	9 US-09-872-852-4	Sequence 4, Appl1
13	234	65.5	44	16 US-10-332-765-27	Sequence 27, Appl1
14	231	64.7	48	14 US-10-091-166B-36	Sequence 36, Appl1

15	231	64.7	48	14 US-10-272-121-36	Sequence 36, Appl1
16	231	64.7	48	14 US-10-409-366-36	Sequence 36, Appl1
17	231	64.7	48	14 US-10-409-532-36	Sequence 36, Appl1
18	231	64.7	49	14 US-10-091-166B-35	Sequence 35, Appl1
19	231	64.7	49	14 US-10-272-121-35	Sequence 35, Appl1
20	231	64.7	49	14 US-10-409-366-35	Sequence 35, Appl1
21	231	64.7	49	14 US-10-409-532-35	Sequence 35, Appl1
22	224	62.7	47	14 US-10-091-166B-38	Sequence 38, Appl1
23	224	62.7	47	14 US-10-272-121-38	Sequence 38, Appl1
24	224	62.7	47	14 US-10-409-366-38	Sequence 38, Appl1
25	224	62.7	47	14 US-10-409-532-38	Sequence 38, Appl1
26	224	62.7	48	14 US-10-091-166B-37	Sequence 37, Appl1
27	224	62.7	48	14 US-10-272-121-37	Sequence 37, Appl1
28	224	62.7	48	14 US-10-409-366-37	Sequence 37, Appl1
29	224	62.7	48	14 US-10-409-532-37	Sequence 37, Appl1
30	220	61.6	41	9 US-09-872-852-3	Sequence 3, Appl1
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34	218	61.1	46	14 US-10-409-532-40	Sequence 40, Appl1
35	218	61.1	47	14 US-10-091-166B-39	Sequence 39, Appl1
36	218	61.1	47	14 US-10-272-121-39	Sequence 39, Appl1
37	218	61.1	47	14 US-10-409-366-39	Sequence 39, Appl1
38	218	61.1	47	14 US-10-409-532-39	Sequence 39, Appl1
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40	210	58.8	45	14 US-10-272-121-42	Sequence 42, Appl1
41	210	58.8	45	14 US-10-409-366-42	Sequence 42, Appl1
42	210	58.8	45	14 US-10-409-532-42	Sequence 42, Appl1
43	210	58.8	46	14 US-10-091-166B-41	Sequence 41, Appl1
44	210	58.8	46	14 US-10-272-121-41	Sequence 41, Appl1
45	210	58.8	46	14 US-10-409-366-41	Sequence 41, Appl1

ALIGNMENTS

RESULT 1
US-10-091-166B-2
Sequence 2, Application US/10091166B
Publication No. US20030143671A1
GENERAL INFORMATION:
APPLICANT: Adler, David A.
APPLICANT: Hollway, James L.
APPLICANT: Baindur, Nand
APPLICANT: Beigel-Orme, Stephanie
APPLICANT: Sheppard, Paul C.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44D1
CURRENT APPLICATION NUMBER: US/10/091.166B
CURRENT FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 09/636,359
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: US 09/344,097
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: US 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: US 60/058,335
PRIOR FILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 65
TYPE: PPT
ORGANISM: Homo sapiens
US-10-091-166B-2

Query Match 100.0%; Score 357; DB 14; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.2e-35;
Matches 65; Conservative 0; Mismatches 0; Gaps 0;

QY 1 MHIHLFLLFLFVLPVPGHGIIINTQKYYCVRGRCALVSLPREQIGKSTRGR 60

Db 1 MRHYLLFALLFLFVPPVGHGIIINTLQKYYCVRGRCVAVLSCLPKKEQIGKSTRGR 60
QY 61 KCCRR 65
61 KCCRR 65

RESULT 2

US-10-272-121-2
Sequence 2, Application US/10272121
Publication No. US20030157638A1
GENERAL INFORMATION:

APPLICANT: Adler, David A.
APPLICANT: Holloway, James L.
APPLICANT: Baidur, Nand
APPLICANT: Beigel-Ome, Stephanie
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44D2
CURRENT APPLICATION NUMBER: US/10/272,121
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 09/636,399
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: US 09/344,097
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: US 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: US 60/058,335
PRIOR FILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 65
TYPE: PRT
ORGANISM: Homo sapiens
US-10-272-121-2

Query Match 100.0%; Score 357; DB 14; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.2e-35;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRHYLLFALLFLFVPPVGHGIIINTLQKYYCVRGRCVAVLSCLPKKEQIGKSTRGR 60
Db 1 MRHYLLFALLFLFVPPVGHGIIINTLQKYYCVRGRCVAVLSCLPKKEQIGKSTRGR 60
QY 61 KCCRR 65
61 KCCRR 65

RESULT 3

US-10-409-366-2
Sequence 2, Application US/10409366
Publication No. US20030166912A1
GENERAL INFORMATION:

APPLICANT: Adler, David A.
APPLICANT: Holloway, James L.
APPLICANT: Baidur, Nand
APPLICANT: Beigel-Ome, Stephanie
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT APPLICATION NUMBER: US/10/409,366
CURRENT FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: US/09/636,399A
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/058,335
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/064,294
PRIOR FILING DATE: 1997-11-05

PRIOR APPLICATION NUMBER: 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/636,399
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 65
TYPE: PRT
ORGANISM: Homo sapiens
US-10-409-366-2

Query Match 100.0%; Score 357; DB 14; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.2e-35;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRHYLLFALLFLFVPPVGHGIIINTLQKYYCVRGRCVAVLSCLPKKEQIGKSTRGR 60
QY 61 KCCRR 65
61 KCCRR 65

RESULT 4

US-10-409-532-2
Sequence 2, Application US/10409532
Publication No. US20030166913A1
GENERAL INFORMATION:

APPLICANT: Adler, David A.
APPLICANT: Holloway, James L.
APPLICANT: Baidur, Nand
APPLICANT: Beigel-Ome, Stephanie
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT APPLICATION NUMBER: US/10/409,532
CURRENT FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: US/09/636,399A
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/058,335
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/636,399
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 65
TYPE: PRT
ORGANISM: Homo sapiens
US-10-409-532-2

Query Match 100.0%; Score 357; DB 14; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.2e-35;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRHYLLFALLFLFVPPVGHGIIINTLQKYYCVRGRCVAVLSCLPKKEQIGKSTRGR 60
Db 1 MRHYLLFALLFLFVPPVGHGIIINTLQKYYCVRGRCVAVLSCLPKKEQIGKSTRGR 60
QY 61 KCCRR 65
61 KCCRR 65

RESULT 5
US-09-917-340-52
Sequence 52, Application US/09917340

Patent No. US20020090369A1
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/290,932
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 52
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-09-917-340-52

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Best Local Similarity 100.0%; Pred. No. 3,3e-35;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MHIHYLFLALFLVLPVPGHGIINTLQKYYCRVGRCAVLSCLPKKEQIGKSTRGR 60

QY 61 KCCRR 65
DB 61 KCCRR 65

RESULT 6
US-09-917-340-72
Sequence 72, Application US/09917340
Patent No. US20020090369A1
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/290,932
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 72
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-09-917-340-72

Query Match 100.0%; Score 357; DB 9; Length 67;
Best Local Similarity 100.0%; Pred. No. 3,3e-35;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MHIHYLFLALFLVLPVPGHGIINTLQKYYCRVGRCAVLSCLPKKEQIGKSTRGR 60
QY 61 KCCRR 65
DB 61 KCCRR 65

RESULT 7
US-09-872-852-2
Sequence 2, Application US/09872852
Patent No. US20020115602A1
GENERAL INFORMATION:
APPLICANT: MCCRAY JR, PAUL B.
APPLICANT: TACK, BRIAN
APPLICANT: JIA, HONG PENG
APPLICANT: SCHUTTE, BRIAN C.
TITLE OF INVENTION: HUMAN BETA-DEFENSIN-3 (HBD-3), A HIGHLY CATIONIC
FILE REFERENCE: IOMA.031US
CURRENT APPLICATION NUMBER: US/09/872,852
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 60/208,792
PRIOR FILING DATE: 2000-06-01
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 67
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-872-852-2

Query Match 100.0%; Score 357; DB 9; Length 67;
Best Local Similarity 100.0%; Pred. No. 3,3e-35;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHIHYLFLALFLVLPVPGHGIINTLQKYYCRVGRCAVLSCLPKKEQIGKSTRGR 60
DB 1 MHIHYLFLALFLVLPVPGHGIINTLQKYYCRVGRCAVLSCLPKKEQIGKSTRGR 60

QY 61 KCCRR 65
DB 61 KCCRR 65

RESULT 8
US-10-091-166B-10
Sequence 10, Application US/10091166B
Publication No. US20030143671A1
GENERAL INFORMATION:
APPLICANT: Adler, David A.
APPLICANT: Holloway, James L.
APPLICANT: Baidur, Nand
APPLICANT: Beigel-Orme, Stephanie
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44DI
CURRENT APPLICATION NUMBER: US/10/091,166B
CURRENT FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 09/636,399
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: US 09/344,097
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: US 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: US 60/058,335
PRIOR FILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-10-091-166B-10


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Query Match      100.0%; Score 357; DB 14; Length 67;
Best Local Similarity 100.0%; Pred. No. 3.3e-35;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHIHYLLFALLFLFVVPVPGHGIINTLQKYYCRVGRGCAVLSCLPKREBQIGKSTRGR 60
DB 1 MHIHYLLFALLFLFVVPVPGHGIINTLQKYYCRVGRGCAVLSCLPKREBQIGKSTRGR 60

QY 61 KCCRR 65
DB 61 KCCRR 65

RESULT 9
US-10-272-121-10
; Sequence 10, Application US/10272121
; Publication No. US20030157638A1
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baidur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44D2
; CURRENT APPLICATION NUMBER: US/10/272,121
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/636,399
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 09/344,097
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: US 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/058,335
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-272-121-10

Query Match      100.0%; Score 357; DB 14; Length 67;
Best Local Similarity 100.0%; Pred. No. 3.3e-35;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHIHYLLFALLFLFVVPVPGHGIINTLQKYYCRVGRGCAVLSCLPKREBQIGKSTRGR 60
DB 1 MHIHYLLFALLFLFVVPVPGHGIINTLQKYYCRVGRGCAVLSCLPKREBQIGKSTRGR 60

QY 61 KCCRR 65
DB 61 KCCRR 65

RESULT 10
US-10-409-366-10
; Sequence 10, Application US/10409366
; Publication No. US20030166912A1
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baidur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/10/409,366
; CURRENT FILING DATE: 2003-04-07
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PRIOR APPLICATION NUMBER: US/09/636,399A
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-409-366-10

Query Match      100.0%; Score 357; DB 14; Length 67;
Best Local Similarity 100.0%; Pred. No. 3.3e-35;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHIHYLLFALLFLFVVPVPGHGIINTLQKYYCRVGRGCAVLSCLPKREBQIGKSTRGR 60
DB 1 MHIHYLLFALLFLFVVPVPGHGIINTLQKYYCRVGRGCAVLSCLPKREBQIGKSTRGR 60

QY 61 KCCRR 65
DB 61 KCCRR 65

RESULT 11
US-10-409-532-10
; Sequence 10, Application US/10409532
; Publication No. US20030166913A1
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baidur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/10/409,532
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US 09/636,399A
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-409-532-10

Query Match      100.0%; Score 357; DB 14; Length 67;
Best Local Similarity 100.0%; Pred. No. 3.3e-35;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MHIHYLLFALLFLFVVPVPGHGIINTLQKYYCRVGRGCAVLSCLPKREBQIGKSTRGR 60

QY 61 KCCRR 65
DB 61 KCCRR 65
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Db 61 KCCR 65

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RESULT 12
US-09-872-852-4
; Sequence 4, Application US/09872852
; Patent No. US20020115602A1
; GENERAL INFORMATION:
; APPLICANT: MCCRAY JR, PAUL B.
; APPLICANT: TACK, BRIAN
; APPLICANT: JIA, HONG PENG
; APPLICANT: SCHUTTE, BRIAN C.
; TITLE OF INVENTION: HUMAN BETA-DEFENSIN-3 (HBD-3), A HIGHLY CATIONIC
; FILE REFERENCE: IOMA-031US
; CURRENT APPLICATION NUMBER: US/09/872,852
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/208,792
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4:
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-872-852-4

Query Match 67.2%; Score 240; DB 9; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.3e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GIINTLQKYYCRVGRGCAVLSCLPKKEQIGKSTGRKCCR 65
Db 1 GIINTLQKYYCRVGRGCAVLSCLPKKEQIGKSTGRKCCR 43

RESULT 13
US-10-332-765-27
; Sequence 27, Application US/10332765
; Publication No. US20040116652A1
; GENERAL INFORMATION:
; APPLICANT: Forstmann, Wolf-Georg
; APPLICANT: Conejo-Garcia, Jose-Ramon
; APPLICANT: Adernann, Knut
; TITLE OF INVENTION: Method for Producing and Using Novel Human Defensins as Biologics
; FILE REFERENCE: 022584us
; CURRENT APPLICATION NUMBER: US/10/332,765
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: DE10033505.5
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-332-765-27

Query Match 65.5%; Score 234; DB 16; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 IINTLQKYYCRVGRGCAVLSCLPKKEQIGKSTGRKCCR 65
Db 1 IINTLQKYYCRVGRGCAVLSCLPKKEQIGKSTGRKCCR 42

RESULT 14
US-10-091-166B-36
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; Sequence 36, Application US/10091166B
; Publication No. US20030143671A1
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baidnur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44D1
; CURRENT APPLICATION NUMBER: US/10/091,166B
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/636,399
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 09/344,097
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: US 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/058,335
; PRIOR FILING DATE: 1997-09-10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (45)...(45)
; OTHER INFORMATION: leucine, isoleucine, valine, phenylalanine, or
; OTHER INFORMATION: methionine
US-10-091-166B-36

Query Match 64.7%; Score 231; DB 14; Length 48;
Best Local Similarity 91.5%; Pred. No. 3e-20;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 19 PGGGIINTLQKYYCRVGRGCAVLSCLPKKEQIGKSTGRKCCR 65
Db 1 PGGGIINTLQKYYCRVGRGCAVLSCLPKKEQIGKSTGRKCCR 47

RESULT 15
US-10-272-121-36
; Sequence 36, Application US/10272121
; Publication No. US20030157638A1
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baidnur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44D2
; CURRENT APPLICATION NUMBER: US/10/272,121
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/636,399
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 09/344,097
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: US 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/058,335
; PRIOR FILING DATE: 1997-09-10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
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LENGTH: 48
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Defensin polypeptide
FEATURE:
NAME/KEY: VARIANT
LOCATION: (45)...(45)
OTHER INFORMATION: leucine, isoleucine, valine, phenylalanine, or
OTHER INFORMATION: methionine
US-10-272-121-36

Query Match 64.7%; Score 231; DB 14; Length 48;
Best Local Similarity 91.5%; Pred. No. 3e-20;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 19 PEGGIIINTLQKYCRVRGGCAVLSCLPKEQIGKCKSTRGRKCCR 65
DB 1 PEGGIIINTLQLYCVRGGCAVLSCLPKEICIGKSTRGRKCCR 47

Search completed: October 13, 2004, 14:54:18
UOD time : 132 secs

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OM protein - protein search, using sw model

Run on: October 13, 2004, 14:42:17 ; Search time 38 Seconds
(without alignments)
113.439 Million cell updates/sec

Title: US-10-272-121-2

Perfect score: 357
Sequence: 1 MRYHYLLPALLFLVPPVPG.....LPKEQIGKSTRKRCRR 65

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	357	100.0	65	4	US-09-636-399A-2
2	357	100.0	67	4	US-09-636-399A-10
3	357	100.0	67	4	US-09-917-340-52
4	357	100.0	67	4	US-09-917-340-72
5	357	100.0	67	4	US-09-636-399A-36
6	357	100.0	67	4	US-09-636-399A-35
7	357	100.0	67	4	US-09-636-399A-37
8	357	100.0	67	4	US-09-636-399A-37
9	357	100.0	67	4	US-09-636-399A-37
10	357	100.0	67	4	US-09-636-399A-37
11	357	100.0	67	4	US-09-636-399A-42
12	357	100.0	67	4	US-09-636-399A-41
13	357	100.0	67	4	US-09-636-399A-44
14	357	100.0	67	4	US-09-636-399A-43
15	357	100.0	67	4	US-09-636-399A-22
16	357	100.0	67	4	US-09-636-399A-21
17	357	100.0	67	4	US-09-636-399A-46
18	357	100.0	67	4	US-09-636-399A-20
19	357	100.0	67	4	US-09-636-399A-45
20	357	100.0	67	4	US-09-636-399A-25
21	357	100.0	67	4	US-09-636-399A-24
22	357	100.0	67	4	US-09-636-399A-48
23	357	100.0	67	4	US-09-636-399A-23
24	357	100.0	67	4	US-09-636-399A-47
25	357	100.0	67	4	US-09-636-399A-28
26	357	100.0	67	4	US-09-636-399A-27
27	357	100.0	67	4	US-09-636-399A-50

28	190	53.2	42	4	US-09-636-399A-26	Sequence 26, Appl
29	190	53.2	42	4	US-09-636-399A-49	Sequence 49, Appl
30	184	51.5	39	4	US-09-636-399A-31	Sequence 31, Appl
31	184	51.5	40	4	US-09-636-399A-30	Sequence 30, Appl
32	184	51.5	40	4	US-09-636-399A-52	Sequence 52, Appl
33	184	51.5	41	4	US-09-636-399A-29	Sequence 29, Appl
34	184	51.5	41	4	US-09-636-399A-51	Sequence 51, Appl
35	179	50.1	38	4	US-09-636-399A-34	Sequence 34, Appl
36	179	50.1	39	4	US-09-636-399A-33	Sequence 33, Appl
37	179	50.1	39	4	US-09-636-399A-54	Sequence 54, Appl
38	179	50.1	40	4	US-09-636-399A-32	Sequence 32, Appl
39	179	50.1	40	4	US-09-636-399A-53	Sequence 53, Appl
40	175	49.0	37	4	US-09-636-399A-14	Sequence 14, Appl
41	175	49.0	38	4	US-09-636-399A-18	Sequence 18, Appl
42	175	49.0	38	4	US-09-636-399A-56	Sequence 56, Appl
43	175	49.0	39	4	US-09-636-399A-19	Sequence 19, Appl
44	175	49.0	39	4	US-09-636-399A-25	Sequence 25, Appl
45	172	48.2	36	4	US-09-636-399A-60	Sequence 60, Appl

ALIGNMENTS

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RESULT 1
US-09-636-399A-2
; Sequence 2, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adier, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baidur, Nand
; APPLICANT: Baisel-Ome, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEPENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-636-399A-2
Query Match      100.0%; Score 357; DB 4; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.9e-37;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 MRYHYLLPALLFLVPPVPGHGIIINTLQYVGRVGRCAVSLCPKEQIGKSTRGR 60
DB      1 MRYHYLLPALLFLVPPVPGHGIIINTLQYVGRVGRCAVSLCPKEQIGKSTRGR 60
QY      61 KCCR 65
DB      61 KCCR 65
RESULT 2
US-09-636-399A-10
; Sequence 10, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adier, David A.
; APPLICANT: Holloway, James L.

```

APPLICANT: Baindur, Nand
APPLICANT: Beigel-Orme, Stephanie
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT APPLICATION NUMBER: US/09/636,399A
CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/058,335
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/636,399
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 10
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-09-636-399A-10

Query Match 100.0%; Score 357; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 2e-37;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLFVLPVPHGGIINTLOKYYCRVGRGCAVLSCLPKKEQIGKSTRGR 60
DB 1 MRIHYLLFALLFLFVLPVPHGGIINTLOKYYCRVGRGCAVLSCLPKKEQIGKSTRGR 60
QY 61 KCCRR 65
DB 61 KCCRR 65

RESULT 3
US-09-917-340-52
Sequence 52, Application US/09917340
Patent No. 6696238
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/290,932
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 52
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-09-917-340-52

Query Match 100.0%; Score 357; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 2e-37;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLFVLPVPHGGIINTLOKYYCRVGRGCAVLSCLPKKEQIGKSTRGR 60
DB 1 MRIHYLLFALLFLFVLPVPHGGIINTLOKYYCRVGRGCAVLSCLPKKEQIGKSTRGR 60
QY 61 KCCRR 65
DB 61 KCCRR 65

RESULT 4
US-09-917-340-72
Sequence 72, Application US/09917340
Patent No. 6696238
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/290,932
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 72
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-09-917-340-72

Query Match 100.0%; Score 357; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 2e-37;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLFVLPVPHGGIINTLOKYYCRVGRGCAVLSCLPKKEQIGKSTRGR 60
DB 1 MRIHYLLFALLFLFVLPVPHGGIINTLOKYYCRVGRGCAVLSCLPKKEQIGKSTRGR 60
QY 61 KCCRR 65
DB 61 KCCRR 65

RESULT 5
US-09-636-399A-36
Sequence 36, Application US/09636399A
Patent No. 657475
GENERAL INFORMATION:
APPLICANT: Adler, David A.
APPLICANT: Holloway, James L.
APPLICANT: Baindur, Nand
APPLICANT: Beigel-Orme, Stephanie
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT APPLICATION NUMBER: US/09/636,399A
CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/058,335
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/636,399
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 36
LENGTH: 48
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Defensin polypeptide
NAME/KEY: VARIANT
LOCATION: (45)...(45)

OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met
US-09-636-399A-36

Query Match 64.7%; Score 231; DB 4; Length 48;
Best Local Similarity 91.5%; Pred. No. 7.8e-22;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 19 PGHGIIINTLQYKYYCRVGRGCAVLSCLPKKEQIGKSTRGKCCR 65
DB 1 PGHGIIINTLQYKYYCRVGRGCAVLSCLPKKEQIGKSTRGKCCR 47

RESULT 6
US-09-636-399A-35
Sequence 35, Application US/09636399A
Patent No. 6576755

GENERAL INFORMATION:
APPLICANT: Adler, David A.
APPLICANT: Holloway, James L.
APPLICANT: Baindur, Nand
APPLICANT: Beigel-Orme, Stephanie
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT FILING DATE: 2000-08-10
CURRENT APPLICATION NUMBER: US/09/636,399A
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/058,335
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 60/064,294
PRIOR FILING DATE: 1998-09-10-150,786
PRIOR APPLICATION NUMBER: 09/150,786
PRIOR FILING DATE: 1998-09-10-150,786
PRIOR APPLICATION NUMBER: 09/636,399
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 35
LENGTH: 49
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Defensin polypeptide
NAME/KEY: VARIANT
LOCATION: (44)...(45)
OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met

US-09-636-399A-35
Query Match 64.7%; Score 231; DB 4; Length 49;
Best Local Similarity 91.5%; Pred. No. 8e-22;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 19 PGHGIIINTLQYKYYCRVGRGCAVLSCLPKKEQIGKSTRGKCCR 65
DB 1 PGHGIIINTLQYKYYCRVGRGCAVLSCLPKKEQIGKSTRGKCCR 47

RESULT 7
US-09-636-399A-38
Sequence 38, Application US/09636399A
Patent No. 6576755
GENERAL INFORMATION:
APPLICANT: Adler, David A.
APPLICANT: Holloway, James L.
APPLICANT: Baindur, Nand
APPLICANT: Beigel-Orme, Stephanie
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT FILING DATE: 2000-08-10
CURRENT APPLICATION NUMBER: US/09/636,399A
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/058,335
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/064,294

PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/636,399
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 38
LENGTH: 47
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Defensin polypeptide
NAME/KEY: VARIANT
LOCATION: (44)...(44)
OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met.

US-09-636-399A-38
Query Match 62.7%; Score 224; DB 4; Length 47;
Best Local Similarity 91.3%; Pred. No. 5.7e-21;
Matches 42; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 20 GHGIIINTLQYKYYCRVGRGCAVLSCLPKKEQIGKSTRGKCCR 65
DB 1 GHGIIINTLQYKYYCRVGRGCAVLSCLPKKEQIGKSTRGKCCR 46

RESULT 8
US-09-636-399A-37
Sequence 37, Application US/09636399A
Patent No. 6576755

GENERAL INFORMATION:
APPLICANT: Adler, David A.
APPLICANT: Holloway, James L.
APPLICANT: Baindur, Nand
APPLICANT: Beigel-Orme, Stephanie
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT FILING DATE: 2000-08-10
CURRENT APPLICATION NUMBER: US/09/636,399A
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/058,335
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/636,399
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 37
LENGTH: 48
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Defensin polypeptide
NAME/KEY: VARIANT
LOCATION: (44)...(44)
OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met

US-09-636-399A-37
Query Match 62.7%; Score 224; DB 4; Length 48;
Best Local Similarity 91.3%; Pred. No. 5.9e-21;
Matches 42; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 20 GHGIIINTLQYKYYCRVGRGCAVLSCLPKKEQIGKSTRGKCCR 65
DB 1 GHGIIINTLQYKYYCRVGRGCAVLSCLPKKEQIGKSTRGKCCR 46

RESULT 9
US-09-636-399A-40

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/ Sequence 40, Application US/09636399A
/ Patent No. 6576755
/ GENERAL INFORMATION:
/ APPLICANT: Adler, David A.
/ APPLICANT: Holloway, James L.
/ APPLICANT: Baidur, Nand
/ APPLICANT: Beigel-Orme, Stephanie
/ APPLICANT: Sheppard, Paul O.
/ TITLE OF INVENTION: NOVEL BETA-DEFENSINS
/ FILE REFERENCE: 97-44C2
/ CURRENT APPLICATION NUMBER: US/09/636,399A
/ PRIOR FILING DATE: 2000-08-10
/ PRIOR APPLICATION NUMBER: 60/058,335
/ PRIOR FILING DATE: 1997-10-09
/ PRIOR APPLICATION NUMBER: 60/064,294
/ PRIOR FILING DATE: 1997-11-05
/ PRIOR APPLICATION NUMBER: 09/150,786
/ PRIOR FILING DATE: 1998-09-10
/ PRIOR APPLICATION NUMBER: 09/636,399
/ PRIOR FILING DATE: 2000-08-10
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 40
/ LENGTH: 46
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Defensin polypeptide
/ NAME/KEY: VARIANT
/ LOCATION: (43)...(43)
/ OTHER INFORMATION: Xaa is Leu, Ile, Phe, Val, or Met
/ US-09-636-399A-40

Query Match          61.1%; Score 218; DB 4; Length 46;
Best Local Similarity 91.1%; Pred. No. 3.2e-20;
Matches 41; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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/ LOCATION: (43)...(43)
/ OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met
/ US-09-636-399A-39

Query Match          61.1%; Score 218; DB 4; Length 47;
Best Local Similarity 91.1%; Pred. No. 3.2e-20;
Matches 41; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      21 HGGIINTLOKYYCRVGRGCAVLSCLPKEBOIGKSTRGRKCCR 65
DB      1 HGGIINTLOLYYCRVGRGCAVLSCLPKEBICIGKSTRGRKCCR 45

RESULT 11
/ Sequence 42, Application US/09636399A
/ Patent No. 6576755
/ GENERAL INFORMATION:
/ APPLICANT: Adler, David A.
/ APPLICANT: Holloway, James L.
/ APPLICANT: Baidur, Nand
/ APPLICANT: Beigel-Orme, Stephanie
/ APPLICANT: Sheppard, Paul O.
/ TITLE OF INVENTION: NOVEL BETA-DEFENSINS
/ FILE REFERENCE: 97-44C2
/ CURRENT APPLICATION NUMBER: US/09/636,399A
/ PRIOR FILING DATE: 2000-08-10
/ PRIOR APPLICATION NUMBER: 60/058,335
/ PRIOR FILING DATE: 1997-10-09
/ PRIOR APPLICATION NUMBER: 60/064,294
/ PRIOR FILING DATE: 1997-11-05
/ PRIOR APPLICATION NUMBER: 09/150,786
/ PRIOR FILING DATE: 1998-09-10
/ PRIOR APPLICATION NUMBER: 09/636,399
/ PRIOR FILING DATE: 2000-08-10
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 42
/ LENGTH: 45
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Defensin polypeptide
/ NAME/KEY: VARIANT
/ LOCATION: (42)...(42)
/ OTHER INFORMATION: Xaa is Leu, Ile, Phe, Val, or Met
/ US-09-636-399A-42

Query Match          58.8%; Score 210; DB 4; Length 45;
Best Local Similarity 90.8%; Pred. No. 3.1e-19;
Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      22 GGIINTLOKYYCRVGRGCAVLSCLPKEBOIGKSTRGRKCCR 65
DB      1 GGIINTLOLYYCRVGRGCAVLSCLPKEBICIGKSTRGRKCCR 44

RESULT 12
/ Sequence 41, Application US/09636399A
/ Patent No. 6576755
/ GENERAL INFORMATION:
/ APPLICANT: Adler, David A.
/ APPLICANT: Holloway, James L.
/ APPLICANT: Baidur, Nand
/ APPLICANT: Beigel-Orme, Stephanie
/ APPLICANT: Sheppard, Paul O.
/ TITLE OF INVENTION: NOVEL BETA-DEFENSINS
/ FILE REFERENCE: 97-44C2
/ CURRENT APPLICATION NUMBER: US/09/636,399A
/ PRIOR FILING DATE: 2000-08-10
/ PRIOR APPLICATION NUMBER: 60/058,335
/ PRIOR FILING DATE: 1997-10-09
```

```

; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (42)...(42)
; OTHER INFORMATION: Xaa is Leu, Ile, Phe, Val, or Met
US-09-636-399A-41
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```

Query Match          58.8%; Score 210; DB 4; Length 46;
Best Local Similarity 90.7%; Pred. No. 3.2e-19;
Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```

QY      22 GGIINTLQKYCRVGRGRCVLSCLPKPEQIGKSTGRKCCR 65
Db      1 GGIINTLQLYYCRVGRGRCVLSCLPKPEQIGKSTGRKCCR 44
```

```

RESULT 13
US-09-636-399A-44
; Sequence 44, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baidnur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (41)...(41)
; OTHER INFORMATION: Xaa is Leu, Ile, Phe, Val, or Met
US-09-636-399A-44
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```

Query Match          57.1%; Score 204; DB 4; Length 44;
Best Local Similarity 90.7%; Pred. No. 1.7e-18;
Matches 39; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```

QY      23 GGIINTLQKYCRVGRGRCVLSCLPKPEQIGKSTGRKCCR 65
Db      1 GGIINTLQLYYCRVGRGRCVLSCLPKPEQIGKSTGRKCCR 43
```

RESULT 14

```

US-09-636-399A-43
; Sequence 43, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baidnur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (41)...(41)
; OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met
US-09-636-399A-43
```

```

Query Match          57.1%; Score 204; DB 4; Length 45;
Best Local Similarity 90.7%; Pred. No. 1.7e-18;
Matches 39; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```

QY      23 GGIINTLQKYCRVGRGRCVLSCLPKPEQIGKSTGRKCCR 65
Db      1 GGIINTLQLYYCRVGRGRCVLSCLPKPEQIGKSTGRKCCR 43
```

```

RESULT 15
US-09-636-399A-22
; Sequence 22, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baidnur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
```


US-09-636-399A-22

Query Match 55.5%; Score 198; DB 4; Length 42;
Best Local Similarity 90.5%; Pred. No. 9e-18;
Matches 38; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 24 IINTLOKYYCVRGRCVLSCLPKESQIGKSTGRKCCR 65
Db 1 IINTLOKYYCVRGRCVLSCLPKESQIGKSTGRKCCR 42

Search completed: October 13, 2004, 14:52:11
Job time : 49 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 14:33:32 / Search time 161 Seconds

(without alignments)
144,829 Million cell updates/sec

Title: US-10-272-121-2

Perfect score: 357
Sequence: 1 MRIHYLLFALLFLVLPVPG.....LPKEQIGKSTRKRCRR 65

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	357	100.0	65	2	AA07243
2	357	100.0	67	2	AA07244
3	357	100.0	67	3	AA07244
4	357	100.0	67	3	AA07244
5	357	100.0	67	5	AA09707
6	357	100.0	67	5	AA09707
7	357	100.0	67	5	AA09707
8	357	100.0	67	5	AA09707
9	357	100.0	67	8	ADN05995
10	240	67.2	45	3	AA010600
11	240	67.2	45	5	AA010600
12	240	67.2	45	5	AA010600
13	220	61.6	41	5	AA010600
14	215	60.2	40	5	AA010600
15	201	56.3	35	6	ABR43502
16	201	56.3	35	6	ABR43502
17	180	50.4	40	7	ADG28620
18	177	49.6	31	5	AA049576
19	177	49.6	31	5	AA049576
20	173	48.5	31	5	AA017765
21	173	48.5	32	3	AA017765
22	163	45.7	35	6	ABR43503
23	163	45.7	35	6	ABR43503
24	138	38.7	27	5	AA017781
25	138	38.7	27	5	AA017781

26	135	37.8	64	5	AA091048	AA091048	Transplan
27	133	37.3	64	2	AA081071	AA081071	Amino aci
28	133	37.3	64	5	AA091049	AA091049	Transplan
29	133	37.3	64	6	AD083836	AD083836	Human DEF
30	133	37.3	64	8	AD075574	AD075574	Marxer ge
31	133	37.3	64	8	ADN04285	ADN04285	Antipsoi
32	133	37.3	64	8	ADN07993	ADN07993	Human bet
33	126	35.3	24	5	AA017774	AA017774	Human bet
34	118	33.1	22	5	AA017772	AA017772	Human bet
35	116.5	32.6	63	4	AA02126	AA02126	Mouse bet
36	112	31.4	19	5	AA017770	AA017770	Human bet
37	108	30.3	64	5	AA086894	AA086894	Prepro-LA
38	108	30.3	64	5	AA090965	AA090965	Transplan
39	106	29.7	64	2	AA024332	AA024332	Tracheal
40	106	29.7	64	2	AA066205	AA066205	Bovine tr
41	106	29.7	64	2	AA066204	AA066204	Bovine tr
42	106	29.7	64	2	AA066205	AA066205	Bovine tr
43	102.5	28.7	63	4	AA02122	AA02122	Mouse zam
44	100	28.0	64	5	AA091052	AA091052	Transplan
45	100	28.0	65	2	AA086896	AA086896	Prepro-LA

ALIGNMENTS

RESULT 1	AA07243	AA07243 standard; protein; 65 AA.
XX	AA07243	
AC	AA07243	
DT	06-JUL-1999	(first entry)
XX		
DE	Beta-defensin family member zamp1.	
XX		
KW	Human; zamp1; beta-defensin; bacterium; fungus; virus; inflammation;	
KW	tissue damage; immune response; AIDS; chemotherapy; melanocortin;	
KW	antibody; ion flux; cytotoxic activity; mammalian cell.	
XX		
OS	Homo sapiens.	
XX		
PN	W09913080-A1.	
XX		
PD	18-MAR-1999.	
XX		
PF	10-SEP-1998;	98MO-US019222.
XX		
PR	10-SEP-1997;	97US-0058335P.
PR	10-SEP-1997;	97US-00926529.
PR	05-NOV-1997;	97US-0064294P.
PR	05-NOV-1997;	97US-00964687.
XX		
PA	(ZYMO) ZYMOGENETICS INC.	
XX		
PI	Adler D, Holloway JL, Bairdur N, Beigel S;	
XX		
DR	WPI, 1999-215064/18.	
XX		
DR	N-PSDB; AAX29985.	
PT	New zamp1 polypeptide and polynucleotide, human beta-defensins - useful	
PT	as diagnostic reagents and for treatment of microbial infections, and	
XX		
XX		
PS	Claim 1, Page 70; 79pp; English.	
XX		
CC	This sequence represents the human zamp1 protein which is a member of the	
CC	beta-defensin protein family. Zamp1 protein is useful as a pharmaceutical	
CC	composition, useful for treatment of e.g. bacterial, fungal and viral	
CC	infections. They are also useful pro-inflammatory, for treating chronic	
CC	tissue damage, and for stimulating the immune response, for treatment of	
CC	AIDS or chemotherapy patients. Zamp1 polypeptides and antibodies are	
CC	useful for studying activity of the melanocortin family, studying ion	
CC	flux in cell culture, and studying cytotoxic activity against mammalian	

CC cells in culture, by incubation with the cells. Zamp1 polypeptides are
 CC especially useful for studying epithelial defensin induction in cell
 CC culture when exposed to pathogenic stimuli

XX Sequence 65 AA;

Query Match 100.0%; Score 357; DB 2; Length 65;
 Best Local Similarity 100.0%; Pred. No. 2.8e-36;
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRHLYLFFALLFLFVPPVPGHGIIINTLOKYYCVRVGRCAVLSCLPKKEIQKSTRGR 60
 DB 1 MRHLYLFFALLFLFVPPVPGHGIIINTLOKYYCVRVGRCAVLSCLPKKEIQKSTRGR 60

QY 61 KCCRR 65
 DB 61 KCCRR 65

RESULT 2

ID AAY07244 standard; protein; 67 AA.

XX AAY07244;

DT 06-JUL-1999 (first entry)

XX Beta-defensin family member zamp1.

KW Human; zamp1; beta-defensin; bacterium; fungus; virus; inflammation;
 KW tissue damage; immune response; AIDS; chemotherapy; melanocortin;
 KW antibody; ion flux; cytotoxic activity; mammalian cell.

OS Homo sapiens.

XX WO913080-A1.

PD 18-MAR-1999.

PF 10-SEP-1998; 98WO-US019222.

XX 10-SEP-1997; 97US-0058335P.

PR 10-SEP-1997; 97US-00926529.

PR 05-NOV-1997; 97US-0064294P.

PR 05-NOV-1997; 97US-00964687.

XX (ZYMO) ZYMOGENETICS INC.

PI Adler D, Holloway JL, Bairdur N, Beigel S;

XX WPI, 1999-215064/18.

DR N-PSDB; AAX29966.

PT New zamp1 polypeptide and polynucleotide, human beta-defensins - useful
 PT as diagnostic reagents and for treatment of microbial infections, and
 PT AIDS.

PS Claim 1; Page 73; 79pp; English.

XX This sequence represents the human zamp1 protein which is a member of the
 CC beta-defensin protein family. Zamp1 protein is useful as a pharmaceutical
 CC composition, useful for treatment of e.g. bacterial, fungal and viral
 CC infections. They are also useful pro-inflammatory, for treating chronic
 CC tissue damage, and for stimulating the immune response, for treatment of
 CC AIDS or chemotherapy patients. Zamp1 polypeptides and antibodies are
 CC useful for studying activity of the melanocortin family, studying ion
 CC flux in cell culture, and studying cytotoxic activity against mammalian
 CC cells in culture, by incubation with the cells. Zamp1 polypeptides are
 CC especially useful for studying epithelial defensin induction in cell
 CC culture when exposed to pathogenic stimuli

XX Sequence 67 AA;

QY 61 KCCRR 65

DB 61 KCCRR 65

QY 61 KCCRR 65

XX Sequence 67 AA;

Query Match 100.0%; Score 357; DB 2; Length 67;
 Best Local Similarity 100.0%; Pred. No. 2.9e-36;
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRHLYLFFALLFLFVPPVPGHGIIINTLOKYYCVRVGRCAVLSCLPKKEIQKSTRGR 60
 DB 1 MRHLYLFFALLFLFVPPVPGHGIIINTLOKYYCVRVGRCAVLSCLPKKEIQKSTRGR 60

QY 61 KCCRR 65
 DB 61 KCCRR 65

RESULT 3

ID AAB10602 standard; protein; 67 AA.

XX AAB10602;

DT 08-JAN-2001 (first entry)

XX Human SAP-3 pre-protein.

KW SAP-2; SAP-3; human; antibiotic; antibacterial; antifungal; antiviral;
 KW treatment; microbial infection; wound dressing; diagnostic reagent.

OS Homo sapiens.

XX WO200046245-A2.

PD 10-AUG-2000.

PF 01-FEB-2000; 2000WO-EP000776.

PR 01-FEB-1999; 99DE-01005128.

PR 08-OCT-1999; 99DE-01049436.

XX (SCHD) SCHERING AG.

PI Christophers E, Harder J, Schroeder J;

XX WPI; 2000-514948/46.

DR N-PSDB; AAX71755.

PT New human antibiotic peptides, useful for treating microbial infections,
 PT particularly when incorporated in wound dressings, also related nucleic
 PT acid.

PS Claim 4; Page 39; 41pp; German.

XX This invention describes the novel active, mature human proteins (I) SAP-
 CC 2 and SAP-3 which have antibiotic, antibacterial, antifungal and
 CC antiviral activity. (I) and their precursors, are useful for treating or
 CC preventing microbial infections (caused by bacteria, fungi or viruses),
 CC particularly where they (or human cells expressing them) are included in
 CC wound dressings, and to produce specific antibodies (Ab) or their
 CC fragments. Ab are used as diagnostic reagents, e.g. to detect a
 CC deficiency of (I) or the presence of a (I) variant. This sequence
 CC represents the human SAP-3 protein described in the method of the
 CC invention

XX Sequence 67 AA;

QY 61 KCCRR 65

DB 61 KCCRR 65

QY 61 KCCRR 65

XX Sequence 67 AA;

QY 61 KCCRR 65

DB 61 KCCRR 65

QY 61 KCCRR 65

XX Sequence 67 AA;

Db 61 KCCR 65

RESULT 4
AAU9707
ID AAU9707 standard; protein; 67 AA.

AC AAU9707;

DT 26-MAR-2002 (first entry)

DE Human beta-defensin-3 (HBD-3).

KW Human; antimicrobial peptide; human beta-defensin-3; HBD-3;
microbial growth; microbial infection; pulmonary infection.

OS Homo sapiens.

PN WO200192309-A2.

PD 06-DEC-2001.

PF 01-JUN-2001; 2001WO-US018057.

PR 01-JUN-2000; 2000US-0208792P.

PS (IOWA) UNITV IOWA RES FOUND.

PI McCreary PB, Tack B, Jia HP, Schutte BC;

DR WPI: 2002-106302/14.

DR N-PSDB; AAS14407.

PT New human beta-defensin 3 peptides and nucleic acids encoding peptides,
useful for treating or preventing microbial growth or infection, or in
gene therapy.

PS Claim 1; Page 96; 110pp; English.

CC The present invention relates to the isolation of a novel antimicrobial
peptide, human beta-defensin-3 (HBD-3). Also described is a method of
inhibiting growth of a microbe by introducing into a host or environment
the antimicrobial peptide of the invention. The peptide is useful for
treating or preventing microbial growth or infections, e.g. pulmonary
infections when administered by inhalation. The peptide can be applied on
a work surface or a surgical instrument for the prevention and/or
suppression of microbial growth. The present sequence represents HBD-3

Sequence 67 AA:

Query Match 100.0%; Score 357; DB 5; Length 67;

Best Local Similarity 100.0%; Pred. No. 2.9e-36;

Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 M R H Y L L F A L L F L V P V P G H G I I N T L Q R Y C R V R G R C A V S C L P K E D I G K S T R G R 60

DB 1 M R H Y L L F A L L F L V P V P G H G I I N T L Q R Y C R V R G R C A V S C L P K E D I G K S T R G R 60

QY 61 KCCR 65

DB 61 KCCR 65

RESULT 5
AAU91016
ID AAU91016 standard; peptide; 67 AA.

AC AAU91016;

DT 05-JUN-2002 (first entry)

DE Transplant media associated defensin peptide #17.

KW Transplant; antimicrobial peptide; pore forming agent;
cell surface receptor binding compound; kidney transplant; cardioplegia;
organ transplant; transplant rejection; defensin.

OS Homo sapiens.

PN WO200209738-A1.

PD 07-FEB-2002.

PF 27-JUL-2001; 2001WO-US023785.

PR 28-JUL-2000; 2000US-0221632P.

PR 17-NOV-2000; 2000US-0249602P.

PR 15-MAY-2001; 2001US-0290932P.

PA (MURP/) MURPHY C J.

PI Murphy CJ, Reid TW, Mcanulty JF;

DR WPI: 2002-268995/31.

PT Media comprising antimicrobial polypeptides or pore forming agents and/or
cell surface receptor binding compounds useful for the storage and
preservation of organs prior to transplant.

PS Claim 8; Page 28; 78pp; English.

CC The invention describes new transplant compositions comprising
antimicrobial polypeptides or pore forming agents and/or cell surface
receptor binding compounds. The media is capable of extending the
preservation period past 72 hours and can provide organs with increased
functionality upon transplant. Animals receiving kidneys stored in the
media of the present invention for either three or four days had serum
creatinine levels of less than half of those observed in control animals
receiving kidneys stored in UW solution (defined in the specification)
alone. Lower serum creatinine levels are indicative of healthier kidneys
and a more preferable prognosis for the transplant patient. The media of
the invention are useful for decreasing the incidence and/or severity of
delayed graft function in patients receiving transplanted kidneys stored
and/or treated in the media. The media may also be used in procedures
such as cardioplegia. It is contemplated that transplant of healthier
organs leads to a decrease in chronic rejection. This sequence represents
an antimicrobial defensin peptide studied in the development of the
transplant media

Sequence 67 AA:

Query Match 100.0%; Score 357; DB 5; Length 67;

Best Local Similarity 100.0%; Pred. No. 2.9e-36;

Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 M R H Y L L F A L L F L V P V P G H G I I N T L Q R Y C R V R G R C A V S C L P K E D I G K S T R G R 60

DB 1 M R H Y L L F A L L F L V P V P G H G I I N T L Q R Y C R V R G R C A V S C L P K E D I G K S T R G R 60

QY 61 KCCR 65

DB 61 KCCR 65

RESULT 6
AAU91036
ID AAU91036 standard; peptide; 67 AA.

AC AAU91036;

DT 05-JUN-2002 (first entry)

DE Transplant media associated defensin peptide #37.

KW Transplant; antimicrobial peptide; pore forming agent;

cell surface receptor binding compound; kidney transplant; cardioplegia;

KW organ transplant; transplant rejection; defensin.
 XX Homo sapiens.
 XX MO200209738-A1.
 FN 07-FEB-2002.
 XX 27-JUL-2001; 2001WO-US023785.
 PF 28-JUL-2000; 2000US-0221633P.
 PR 17-NOV-2000; 2000US-0248603P.
 PR 15-MAY-2001; 2001US-0290932P.
 XX (MURP/) MURPHY C J.
 XX Murphy CJ, Reid TW, Meanlty JF;
 PI WPI, 2002-268995/31.
 DR
 XX
 XX Media comprising antimicrobial polypeptides or pore forming agents and/or
 PT cell surface receptor binding compounds useful for the storage and
 PR preservation of organs prior to transplant.
 XX
 PS Claim 8; Page 30; 78pp; English.
 XX
 XX The invention describes new transplant compositions comprising
 CC antimicrobial polypeptides or pore forming agents and/or cell surface
 CC receptor binding compounds. The media is capable of extending the
 CC preservation period past 72 hours and can provide organs with increased
 CC functionality upon transplant. Animals receiving kidneys stored in the
 CC media of the present invention for either three or four days had serum
 CC creatinine levels of less than half of those observed in control animals
 CC receiving kidneys stored in UW solution (defined in the specification)
 CC alone. Lower serum creatinine levels are indicative of healthier kidneys
 CC and a more preferable prognosis for the transplant patient. The media of
 CC the invention are useful for decreasing the incidence and/or severity of
 CC delayed graft function in patients receiving transplanted kidneys stored
 CC and/or treated in the media. The media may also be used in procedures
 CC such as cardioplegia. It is contemplated that transplant of healthier
 CC organs leads to a decrease in chronic rejection. This sequence represents
 CC an antimicrobial defensin peptide studied in the development of the
 CC transplant media
 CC
 SQ Sequence 67 AA;
 Query Match 100.0%; Score 357; DB 5; Length 67;
 Best Local Similarity 100.0%; Pred. No. 2.9e-36;
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 QY 1 M R I H I L F A L L F L F V P V P G H G I I N T L K Y Y C R V G G C A V L S C P K E Q I G K S T R R 60
 DB 1 M R I H I L F A L L F L F V P V P G H G I I N T L K Y Y C R V G G C A V L S C P K E Q I G K S T R R 60
 QY 61 K C C R R 65
 DB 61 K C C R R 65
 DE Human beta-defensin-3 derivative #3.
 XX
 XX Human, beta-defensin-3; hBD-3; bacterial infection; gene therapy;
 KW respiratory system; cystic fibrosis; inflammation; urogenital tract;
 KW antibacterial; fungicide; cytostatic; antiinflammatory; antitumor;
 KW gastrointestinal tract; septicemia; apoptosis induction; cancer.

XX	Homo sapiens.
OS	
FN	W0300240512-A2.
PD	
FD	23-MAY-2002.
XX	
PF	14-NOV-2001; 2001WO-EP013174.
XX	
PR	14-NOV-2000; 2000DE-01056365.
XX	
PR	30-MAR-2001; 2001DE-01016220.
XX	
PA	(IPFP-) IPF PHARM GMBH.
XX	
PI	Fortsmann W, Kluever E, Conejo-Garcia J, Adermann K, Bals R;
PI	Maegert H;
XX	
DR	WPI; 2002-435959/46.
PT	New human beta-defensin 3, useful for treating or preventing microbial
PT	infection and tumors, also related nucleic acid.
XX	
PS	Claim 2, Page 23; 36pp; German.
XX	
CC	The present invention relates to human beta-defensin-3 (hBD-3) and its
CC	derivatives. The peptide, its coding sequence and vectors containing the
CC	coding sequence are useful in (gene) therapy and diagnostics, especially
CC	for preventing or treating a wide range of microbial infections
CC	(particularly Bartholderia cepacia and Pseudomonas aeruginosa in the
CC	respiratory tract, especially in cases of cystic fibrosis, and
CC	Helicobacter pylori, also inflammatory diseases of the gastrointestinal
CC	and urogenital tracts, sepsis and yeast infections), and for inducing
CC	apoptosis for treating malignant melanoma and tumours. The present
CC	sequence is a derivative of human BD-3
XX	
SQ	Sequence 67 AA;
Query Match	100.0%; Score 357; DB 5; Length 67;
Best Local Similarity	100.0%; Pred. No. 2, 9e-36;
Matches	65; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Dy	1 MRIHYLLFALLFLPLVEVPVGHGIIINTLOKYYCVRGGRCALVSLCPKXEDIGKSTGR 60 1 MRIHYLLFALLFLPLVEVPVGHGIIINTLOKYYCVRGGRCALVSLCPKXEDIGKSTAGR 60
Dd	61 KCGR 65 61 KCGR 65
Db	61 KCGR 65
RESULT 8	
ID	ADN05995 standard; protein; 67 AA.
AC	ADN05995;
DT	01-JUN-2004 (first entry)
XX	
DE	Antiproliferative protein sequence #1157.
XX	
KW	antiproliferative; gene therapy; psoriasis; diagnosis.
XX	
OS	Homo sapiens.
XX	
PN	W02004028479-A2.
XX	
PD	08-APR-2004.
XX	
PF	25-SEP-2003; 2003WO-US030807.
XX	
PR	25-SEP-2002; 2002US-0414006P.
XX	
PA	(GETH) GENENTECH INC.

Best Local Similarity 100.0%; Pred. No. 5.2e-22; Indels 0; Gaps 0;
Matches 43; Conservative 0; Mismatches 0;

QY 23 GIINTLOKYYCVRGRCVAVLSCLPKKEQIGKSTRGRKCCR 65
DB 1 GIINTLOKYYCVRGRCVAVLSCLPKKEQIGKSTRGRKCCR 43

RESULT 11

AAU09709 ID AAU09709 standard; protein; 45 AA.

AAU09709;

26-MAR-2002 (first entry)

Human beta-defensin-3 (HBD-3) mature protein sequence #2.

Human; antimicrobial peptide; human beta-defensin-3; HBD-3; microbial growth; microbial infection; pulmonary infection.

Homo sapiens.

WO200192309-A2.

06-DEC-2001.

01-JUN-2001; 2001WO-US018057.

01-JUN-2000; 2000US-0208792P.

(IOWA) UNIV IOWA RES FOUND.

McCraty PB, Tack B, Jia HP, Schutte BC;

WPI; 2002-106302/14.

New human beta-defensin 3 peptides and nucleic acids encoding peptides, useful for treating or preventing microbial growth or infection, or in gene therapy.

Claim 29; Page 98; 110pp; English.

The present invention relates to the isolation of a novel antimicrobial peptide, human beta-defensin-3 (HBD-3). Also described is a method of inhibiting growth of a microbe by introducing into a host or environment the antimicrobial peptide of the invention. The peptide is useful for treating or preventing microbial growth or infections, e.g. pulmonary infections when administered by inhalation. The peptide can be applied on a work surface or a surgical instrument for the prevention and/or suppression of microbial growth. The present sequence represents HBD-3 mature protein sequence #2

Sequence 45 AA;

Query Match 67.2%; Score 240; DB 5; Length 45;
Best Local Similarity 100.0%; Pred. No. 5.2e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GIINTLOKYYCVRGRCVAVLSCLPKKEQIGKSTRGRKCCR 65
DB 1 GIINTLOKYYCVRGRCVAVLSCLPKKEQIGKSTRGRKCCR 43

RESULT 12

AA017767 ID AA017767 standard; peptide; 45 AA.

AA017767;

30-AUG-2002 (first entry)

Human beta-defensin-3 derivative #2.

Human; beta-defensin-3; HBD-3; bacterial infection; gene therapy; respiratory system; cystic fibrosis; inflammation; urogenital tract; antimicrobial; fungicide; cytostatic; antiinflammatory; anticancer; gastrointestinal tract; septicemia; apoptosis induction; cancer.

Homo sapiens.

WO200240512-A2.

23-MAY-2002.

14-NOV-2001; 2001WO-EP013174.

14-NOV-2000; 2000DE-01056365.

30-MAR-2001; 2001DE-01016220.

(IPFP-) IFF PHARM GMBH.

Forsmann W, Kluever E, Conejo-Garcia J, Adermann K, Bals R, Maegert H;

WPI; 2002-435959/46.

New human beta-defensin 3, useful for treating or preventing microbial infection and tumors, also related nucleic acid.

Claim 2; Page 23; 36pp; German.

The present invention relates to human beta-defensin-3 (HBD-3) and its derivatives. The peptide, its coding sequence and vectors containing the coding sequence are useful in (gene) therapy and diagnosis, especially for preventing or treating a wide range of microbial infections (particularly Burkholderia cepacia and pseudomonas aeruginosa in the respiratory tract, especially in cases of cystic fibrosis, and Helicobacter pylori, also inflammatory diseases of the gastrointestinal tract and urogenital tracts, sepsis and yeast infections), and for inducing apoptosis for treating malignant melanoma and tumours. The present sequence is a derivative of human BD-3

Sequence 45 AA;

Query Match 67.2%; Score 240; DB 5; Length 45;
Best Local Similarity 100.0%; Pred. No. 5.2e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GIINTLOKYYCVRGRCVAVLSCLPKKEQIGKSTRGRKCCR 65
DB 1 GIINTLOKYYCVRGRCVAVLSCLPKKEQIGKSTRGRKCCR 43

RESULT 13

AAU09708 ID AAU09708 standard; protein; 41 AA.

AAU09708;

26-MAR-2002 (first entry)

Human beta-defensin-3 (HBD-3) mature protein sequence #1.

Human; antimicrobial peptide; human beta-defensin-3; HBD-3; microbial growth; microbial infection; pulmonary infection.

Homo sapiens.

WO200192309-A2.

06-DEC-2001.

01-JUN-2001; 2001WO-US018057.

01-JUN-2000; 2000US-0208792P.

XX (IOWA) UNIV IOWA RES FOUND.
 PA
 XX
 XX McCray PB, Tack B, Jia HP, Schutte BC;
 PI
 XX WPI; 2002-106302/14.
 DR
 XX
 XX New human beta-defensin 3 peptides and nucleic acids encoding peptides,
 PT useful for treating or preventing microbial growth or infection, or in
 PT gene therapy.
 XX
 XX Claim 28; Page 97; 110pp; English.
 PS
 XX The present invention relates to the isolation of a novel antimicrobial
 CC peptide, human beta-defensin-3 (HBD-3). Also described is a method of
 CC inhibiting growth of a microbe by introducing into a host or environment
 CC the antimicrobial peptide of the invention. The peptide is useful for
 CC treating or preventing microbial growth or infections, e.g. pulmonary
 CC infections when administered by inhalation. The peptide can be applied on
 CC a work surface or a surgical instrument for the prevention and/or
 CC suppression of microbial growth. The present sequence represents HBD-3
 CC mature protein sequence #1
 CC
 SQ Sequence 41 AA;
 Query Match 61.6%; Score 220; DB 5; Length 41;
 Best Local Similarity 100.0%; Pred. No. 1,4e-19;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 27 TLQKYYCRVGRGCAVLSCLPKKEOIGKSTRGKCCR 65
 Db 1 TLQKYYCRVGRGCAVLSCLPKKEOIGKSTRGKCCR 39
 RESULT 14
 AA017766
 ID AA017766 standard; peptide; 40 AA.
 XX
 AC AA017766;
 XX
 DT 30-AUG-2002 (first entry)
 XX
 DE Human beta-defensin-3 derivative #1.
 XX
 XX Human; beta-defensin-3; hbd-3; bacterial infection; gene therapy;
 KW respiratory system; cystic fibrosis; inflammation; urogenital tract;
 KW antibacterial; fungicide; cytostatic; antiinflammatory; anticancer;
 KW gastrointestinal tract; septicemia; apoptosis induction; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200240512-A2.
 XX
 PD 23-MAY-2002.
 XX
 PF 14-NOV-2001; 2001WO-EP013174.
 XX
 PR 14-NOV-2000; 2000DE-01056365.
 PR 30-MAR-2001; 2001DE-01016220.
 XX
 XX (IPPP-) IPF PHARM GMBH.
 PA
 XX Forstmann W, Kluver E, Conejo-Garcia J, Adernann K, Bals R;
 PI Maegert H;
 XX
 XX WPI; 2002-435959/46.
 DR
 XX New human beta-defensin 3, useful for treating or preventing microbial
 PT infection and tumors, also related nucleic acid.
 XX
 XX Claim 2; Page 23; 36pp; German.
 PS
 XX The present invention relates to human beta-defensin-3 (hbd-3) and its

CC derivatives. The peptide, its coding sequence and vectors containing the
 CC coding sequence are useful in (gene) therapy and diagnosis, especially
 CC for preventing or treating a wide range of microbial infections
 CC (particularly Burkholderia cepacia and Pseudomonas aeruginosa in the
 CC respiratory tract, especially in cases of cystic fibrosis), and
 CC Helicobacter pylori, also inflammatory diseases of the gastrointestinal
 CC and urogenital tracts, sepsis and yeast infections), and for inducing
 CC apoptosis for treating malignant melanoma and tumours. The present
 CC sequence is a derivative of human BD-3
 CC
 SQ Sequence 40 AA;
 Query Match 60.2%; Score 215; DB 5; Length 40;
 Best Local Similarity 100.0%; Pred. No. 5,6e-19;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 28 LQKYYCRVGRGCAVLSCLPKKEOIGKSTRGKCCR 65
 Db 1 LQKYYCRVGRGCAVLSCLPKKEOIGKSTRGKCCR 38
 RESULT 15
 ABR43502
 ID ABR43502 standard; peptide; 35 AA.
 XX
 AC ABR43502;
 XX
 DT 16-JUN-2003 (first entry)
 XX
 DE Human beta-defensin peptide DEFB3 SEQ ID NO:7.
 XX
 KW Beta-defensin; antimicrobial; antibacterial; vaccine; gene therapy;
 KW infection; antibiotic; chromosome 8p23-p22.
 XX
 OS Homo sapiens.
 XX
 PN WO2003024592-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 23-SEP-2002; 2002WO-US030106.
 XX
 PR 21-SEP-2001; 2001US-0323991P.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 PA
 XX McCray PB, Schutte BC, Jia HP, Casavant TJ, Welch MJ;
 PI WPI; 2003-354585/33.
 DR
 XX New antimicrobial peptides, beta-defensin, useful for preventing
 PT microbial growth, for treating pulmonary infections, for reducing
 PT resistance to antimicrobials and antibiotics, and for inhibiting
 PT multidrug resistant bacteria.
 XX
 PS Claim 1; Page 78; 125pp; English.
 XX
 XX ABR43496 to ABR43577 represent beta-defensin antimicrobial peptides (I).
 CC (I) have antibacterial activity and can be used in vaccines, and in gene
 CC therapy. (II) can be used for preventing microbial growth, for treating
 CC infections (e.g. pulmonary infections), for reducing resistance to
 CC antimicrobials and antibiotics, and for inhibiting multidrug resistant
 CC bacteria. The antimicrobial peptides may be included in food
 CC preparations, pharmaceutical preparations, medicinal and pharmaceutical
 CC products, cosmetic products, hygienic products, cleaning products and
 CC cleaning agents, as well as to any material to which the peptides could
 CC be sprayed on or adhered to where inhibition of microbial growth on such
 CC material is desired. The antimicrobial peptides and nucleic acids
 CC encoding them may be used in gene therapy. ABR43578 to ABR43610 represent
 CC human beta-defensin peptides given in an example from the present
 CC invention
 XX
 SQ Sequence 35 AA;

Wed Oct 13 15:08:00 2004

us-10-272-121-2.rag

Page 8

Query Match 56.3%; Score 201; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.6e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 31 YYCVRGGRCVAVLSCLPKKEQIGKSTRGRKCCR 65
1 YYCVRGGRCVAVLSCLPKKEQIGKSTRGRKCCR 35
Search completed: October 13, 2004, 14:47:11
Job time : 163 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 14:50:44 ; Search time 193 Seconds
(without alignments)
193.779 Million cell updates/sec

Title: US-10-272-121-2

Perfect score: 65
Sequence: 1 MRHYLLFALLFLVLPVPG.....LPKEEQIGCKSTRKCCRR 65

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	65	100.0	67 1 D103 HUMAN	P81534 homo sapien
2	47	72.3	67 2 Q7PCK4	Q7PCK4 papio anubi
3	43	66.2	64 1 D103 PANTR	Q951d2 pan troglod
4	15	23.1	67 2 Q6SC68	Q6SC68 sus scrofa
5	15	23.1	67 2 AAR88759	AAR88759 sus scrofa
6	9	13.8	63 1 BD03 MOUSE	Q9w10 mus musculu
7	9	13.8	64 2 Q9B9V9	Q9B9V9 mus musculu
8	9	13.8	67 1 BD01 CHILA	P83943 chinchilla
9	8	12.3	60 2 Q91V82	Q91V82 mus musculu
10	8	12.3	60 2 Q8R556	Q8R556 mus musculu
11	8	12.3	63 1 BD02 RAT	Q86514 rattus norv
12	8	12.3	63 1 BD04 MOUSE	P82019 mus musculu
13	8	12.3	67 2 Q7TIN9	Q7TIN9 mus musculu
14	8	12.3	516 2 Q7PIL5	Q7PIL5 chromobacte
15	7	10.8	51 1 YFMN BACSU	Q06472 bacillus su
16	7	10.8	56 2 Q8R937	Q8R937 thermoanaer
17	7	10.8	63 2 Q91VD6	Q91VD6 mus musculu
18	7	10.8	78 2 Q6XIU6	Q6XIU6 feildmannia
19	7	10.8	78 2 AAR26965	AAR26965 feildmanni
20	7	10.8	87 2 Q751P3	Q751P3 nesiohellx
21	7	10.8	87 2 Q75216	Q75216 euhadra lat
22	7	10.8	87 2 Q75222	Q75222 euhadra lat
23	7	10.8	87 2 BAC99163	BAC99163 euhadra 1
24	7	10.8	87 2 BAC99169	BAC99169 euhadra 1
25	7	10.8	87 2 BAC99282	BAC99282 nesiohell
26	7	10.8	91 2 Q76C85	Q76C85 human adeno
27	7	10.8	91 2 Q76EL4	Q76EL4 human adeno
28	7	10.8	91 2 Q77V93	Q77V93 human adeno
29	7	10.8	91 2 Q77B68	Q77B68 human adeno
30	7	10.8	91 2 Q801V6	Q801V6 human adeno
31	7	10.8	91 2 Q91CD4	Q91CD4 human adeno

32	7	10.8	91 2 Q9JFL9	Q9JFL9 human adeno
33	7	10.8	91 2 Q9JFM2	Q9JFM2 human adeno
34	7	10.8	91 2 Q9JFM5	Q9JFM5 human adeno
35	7	10.8	91 2 BAC92701	BAC92701 human ade
36	7	10.8	91 2 BAC97855	BAC97855 human ade
37	7	10.8	101 1 QY02 CATRO	P25923 catnaranthu
38	7	10.8	124 2 Q6WZ11	Q6WZ11 homo sapien
39	7	10.8	124 2 CAE46051	CAE46051 homo sapi
40	7	10.8	125 1 NEU1 HUMAN	P01178 homo sapien
41	7	10.8	125 2 AAB65144	AAB65144 homo sapi
42	7	10.8	173 2 Q12408	Q12408 saccharomyc
43	7	10.8	179 2 Q7QX80	Q7QX80 giardia lam
44	7	10.8	201 2 Q9CDB0	Q9CDB0 mycobacteri
45	7	10.8	201 2 Q92R12	Q92R12 thalobium m

ALIGNMENTS

RESULT 1
D103_HUMAN
ID D103_HUMAN STANDARD; PRT; 67 AA.
AC P81534; Q8NFG6; Q9NPF6;
DT 16-OCT-2001 (Ref. 40, Created)
DT 16-OCT-2001 (Ref. 40, Last sequence update)
DT 01-OCT-2004 (Ref. 45, Last annotation update)
DE Beta-defensin 103a precursor (Beta-defensin 3) (DEFB-3) (BD-3) (HBD-3)
DE (HBD3) (Defensin like protein).
GN Name=DEFB103A; Synonyms=DEFB103, DEFB3, BD3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
[1]
RN SEQUENCE FROM N.A., SEQUENCE OF 23-67, FUNCTION, TISSUE SPECIFICITY,
RP INDUCTION, AND MASS SPECTROMETRY.
RC Tissue=Keratinocytes, Lung epithelial cells, and Tracheal epithelium;
RA MEDLINE=21101950; PubMed=11085990; DOI=10.1074/jbc.M008557200;
RX Harder J., Barrels J., Christophers E., Schroeder J.-M.;
RT "Isolation and characterization of human beta-defensin-3, a novel
RT human inducible peptide antibiotic.";
RL J. Biol. Chem. 276:5707-5713(2001).
[2]
RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
RP MEDLINE=2158153; PubMed=11702237; DOI=10.1007/s004410100433;
RX Conejo-Garcia J.-R., Jaumann F., Schulz S., Krause A.,
RA Rodriguez-Jimenez J., Forsmann U., Adernann K., Kluever E.,
RA Vogeleiter C., Becker D., Hedrich R., Forsmann W.-G., Bales R.;
RT "Identification of a novel, multifunctional beta-defensin (human beta-
RT defensin 3) with specific antimicrobial activity. Its interaction with
RT plasma membranes of Xenopus oocytes and the induction of macrophage
RT chemotraction.";
RL Cell Tissue Res. 306:257-264(2001).
[3]
RN SEQUENCE FROM N.A.
RP MEDLINE=21125233; PubMed=11223260; DOI=10.1016/S0378-1119(00)00569-2;
RX Jia H.-P., Schutte B.C., Schudy A., Linzmeier R., Gutthiller J.M.,
RA Johnson G.K., Jack B.F., Mitros J.P., Rosenthal A., Ganz T.,
RA McCray P.B., Jr.;
RT "Discovery of new human defensins using a genomics-based approach.";
RL Gene 263:211-216(2001).
[4]
RN SEQUENCE FROM N.A.
RP Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
[5]
RN SEQUENCE FROM N.A.
RA Adler D.A., Diamond G., Sheppard P., Holloway J., Presnell S.,
RA Jaepens S., Whitmore T., Fox B., Goelink J., Rixon M., Cao Z.,
RA Haldeman B., O'Hara P.;
RT "EST and genomic database mining yield novel human and mouse beta-
RT defensins.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN SEQUENCE FROM N.A.
 RC TISSUE=Tonsil;
 RA Chen S., He F., Li R.;
 RT "Cloning and expression of Chinese human beta defensin-3."
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP STRUCTURE BY NMR OF 23-67.
 RX MEDLINE=21864161; PubMed=11741980; DOI=10.1074/jbc.M108830200;
 RA Schibli D.J., Hunter H.N., Aseyev V., Stanner T.D., Wiencek J.M.,
 RA McCrory P.B., Jr., Tack B.F., Vogel H.J.;
 RT "The solution structures of the human beta-defensins lead to a better
 RT understanding of the potent bactericidal activity of HBD3 against
 RT *Staphylococcus aureus*."
 RL J. Biol. Chem. 277:8279-8289(2002).
 CC -1- FUNCTION: Exhibits antimicrobial activity against Gram-positive
 CC bacteria *S. aureus* and *S. pyogenes*, Gram-negative bacteria
 CC *P. aeruginosa* and *E. coli* and the yeast *C. albicans*. Kills
 CC multiresistant *S. aureus* and vancomycin-resistant *E. faecium*. No
 CC significant hemolytic activity was observed.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Highly expressed in skin and tonsils, and to a
 CC lesser extent in trachea, uterus, kidney, thymus, adenoid, pharynx
 CC and tongue. Low expression in salivary gland, bone marrow, colon,
 CC stomach, polyp and larynx. No expression in small intestine.
 CC -1- INDUCTION: By infection of bacteria and by interferon gamma.
 CC -1- MASS SPECTROMETRY: MW=5154.59; METHOD=Electrospray; RANGE=23-67;
 CC NOTE=Ref.1
 CC -1- SIMILARITY: Belongs to the beta-defensin family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC or send an email to license@sib-sib.ch).
 CC
 DR EMBL: AJ237673; CA030971.1;
 DR EMBL: AF295370; AAG02237.1;
 DR EMBL: AF217245; AAF73853.1;
 DR EMBL: AB037972; BAB40572.1;
 DR EMBL: AF031470; AAG22030.1;
 DR EMBL: AF516673; AAM62424.1;
 DR PDB: 1K16; NMR: A=23-66.
 DR Genew: HGNC:15967; DEFB103A.
 DR MTM: 606611;
 DR GO: GO:0005576; C:extracellular; NMS.
 DR GO: GO:0006965; P:anti-Gram-positive bacterial polypeptide in. . .; TMS.
 DR InterPro: IPR001855; Defensin_beta.
 DR Pfam: PF00711; Defensin_beta; 1.
 KM 3D-structure; Antibiotic; Direct protein sequencing; Signal.
 FT SIGNAL 1 22
 FT CHAIN 1 67
 FT DISULFID 33 62
 FT DISULFID 40 55
 FT DISULFID 45 63
 FT DISULFID 45 63
 FT CONFLICT 29 31 C -> R (in Ref. 6).
 FT TURN 32 36
 FT HELIX 32 36
 FT STRAND 39 41
 FT TURN 47 48
 FT STRAND 49 53
 FT STRAND 49 53
 FT STRAND 61 65
 SQ SEQUENCE 67 AA; 7697 MW; 54266DE1C9D4B65 CRC64;
 Query Match 100.0%; Score 65; DB 1; Length 67;
 Best Local Similarity 100.0%; Pred. No. 2,3e-56;
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRLHYLLFALLFLFVVPBGHGIINTLQKYYRVRGRCVAVSCLPKEEQIGKSTRGR 60
 DB 1 MRLHYLLFALLFLFVVPBGHGIINTLQKYYRVRGRCVAVSCLPKEEQIGKSTRGR 60

QY 61 KCCRR 65
 DB 61 KCCRR 65
 RESULT 2
 ID 07PCK4 PRELIMINARY; PRT; 67 AA.
 AC 07PCK4;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE DEFB103-like protein (Fragment).
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Papio.
 OX NCBI_Taxid=9555;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22619651; PubMed=12734011;
 RA Semple C.A., Rolfe M., Dorn J.R.;
 RT "Duplication and selection in the evolution of primate beta-defensin
 RT genes."
 RL Genome Biol. 4:R31-R31(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Semple C.A.M., Rolfe M., Dorn J.R.;
 RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- MISCELLANEOUS: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
 DR EMBL: BK00557; DA01350.1;
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0006952; P:defense response; IEA.
 DR GO: GO:0009613; P:response to pest/pathogen/parasite; IEA.
 DR InterPro: IPR01855; Defensin_beta.
 DR Pfam: PF00711; Defensin_beta; 1.
 FT NON_TER 67 67
 SQ SEQUENCE 67 AA; 7669 MW; 543FE0570B5D4B65 CRC64;
 Query Match 72.3%; Score 47; DB 2; Length 67;
 Best Local Similarity 100.0%; Pred. No. 1,4e-38;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 19 PFGHGIINTLQKYYRVRGRCVAVSCLPKEEQIGKSTRGRKCCRR 65
 DB 19 PFGHGIINTLQKYYRVRGRCVAVSCLPKEEQIGKSTRGRKCCRR 65
 RESULT 3
 ID D103_PANTR STANDARD; PRT; 64 AA.
 AC 095ID2;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Beta-defensin 103A precursor (Beta-defensin 3) (DEFB-3) (BD-3) (Fragment).
 GN Name=DEFB103A; Synonyms=DEFB103, DEFB3;
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
 OX NCBI_Taxid=9596;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Dulte L.A., Langemann J.A.W., Ravensbergen B., Paltansing S.,
 RA Verreken R.A.W., Hiemstra P.S., Thomas A.W., Nibbering P.H.;
 RT "Expression of chimpanzee (Pan troglodytes) beta-defensin-3."
 RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Exhibits antimicrobial activity against Gram-positive
 CC and Gram-negative bacteria (By similarity).

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CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the beta-defensin family.
CC -----
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CC -----
CC EMBL; AY033883; AAK61549.1; -.
CC InterPro; IPR001855; Defensin_beta.
CC Pfam; PF00711; Defensin_beta; 1.
CC Antibiocic; Signal.
CC SIGNAL 1 22 By similarity.
CC CHAIN 23 >64 Beta-defensin 103A.
CC DISULFID 33 62 By similarity.
CC DISULFID 40 55 By similarity.
CC DISULFID 45 63 By similarity.
CC NON_TER 64 64
CC SEQUENCE 64 AA; 7299 MW; 01C90D4B60218DC8 CRC64;
SQ
Query Match 66.2%; Score 43; DB 1; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRLHYLLFALLFLFVPEVPGHGIINTLQKYYCRVGRCAVL 43
DB 1 MRLHYLLFALLFLFVPEVPGHGIINTLQKYYCRVGRCAVL 43
RESULT 4
Q6SC68 PRELIMINARY; PRT; 67 AA.
AC Q6SC68;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Prepro-beta-defensin 3.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Sang Y., Zhang G., Ross C.R., Blecha F.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY460575; AAR88759.1; -.
DR EMBL; AY460575; AAR88759.1; -.
SQ SEQUENCE 67 AA; 7790 MW; 6BC28264846572AC CRC64;
QY Query Match 23.1%; Score 15; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 6.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 MRLHYLLFALLFLF 15
DB 1 MRLHYLLFALLFLF 15
RESULT 5
AAR88759 PRELIMINARY; PRT; 67 AA.
AC AAR88759;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Prepro-beta-defensin 3.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_TaxID=9823;
RN [1]

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RP SEQUENCE FROM N.A.
RA Sang Y., Zhang G., Ross C.R., Blecha F.;
RL "Characterization of porcine beta-defensin 3 and synergistic effect of
RL porcine beta-defensin 1, 2 and 3."
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY460575; AAR88759.1; -.
DR EMBL; AY460575; AAR88759.1; -.
SQ SEQUENCE 67 AA; 7790 MW; 6BC28264846572AC CRC64;
QY Query Match 23.1%; Score 15; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 6.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 MRLHYLLFALLFLF 15
DB 1 MRLHYLLFALLFLF 15
RESULT 6
BD03 MOUSE
ID BD03 MOUSE STANDARD; PRT; 63 AA.
AC Q9WTD0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-defensin 3 precursor (BD-3) (MBD-3).
GN Name=Defb3; Synonyms=Bd3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.; FUNCTION, INDUCTION, AND TISSUE SPECIFICITY.
RC STRAIN=C57BL/6; TISSUE=Lung;
RC MEDLINE=99307216; PubMed=10377137;
RA Bals R., Wang X., Meegalla R.L., Wattler S., Weiner D.J., Nehls M.C.,
RA Wilson J.M.;
RT "Mouse beta-defensin 3 is an inducible antimicrobial peptide expressed
RT in the epithelia of multiple organs."
RL Infect. Immun. 67:3542-3547(1999).
RN [2]
RP TISSUE SPECIFICITY.
RC STRAIN=C57BL/6, 129/SvJ, and FVB; TISSUE=Lung;
RC MEDLINE=20517883; PubMed=10923379;
RA Jia H.P., Mowk S.A., Schutte B.C., Lee S.K., Vivado A., Tack B.F.,
RA Bevins C.L., McCray P.B. Jr.;
RT "A novel murine beta-defensin expressed in tongue, esophagus, and
RT trachea."
RL J. Biol. Chem. 275:33314-33320(2000).
RN [1]
RP FUNCTION: Antimicrobial activity against Gram-negative bacteria
E.coli and P.aeruginosa.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Highest expression in salivary glands,
CC epidiidymis, ovary and pancreas and to a lesser extent in lung,
CC liver and brain. Low or no expression in skeletal muscle and
CC tongue.
CC -1- INDUCTION: By bacterial infection.
CC -1- SIMILARITY: Belongs to the beta-defensin family. LAP/TAP
CC subfamily.
CC -----
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CC -----
CC EMBL; AF093245; AAD29573.1; -.
CC EMBL; AF092929; AAD29572.1; -.
CC HSSP; O15263; 1B40.
CC MGD; MGI:1351612; Defb3.
CC InterPro; IPR001855; Defensin_beta.
CC InterPro; IPR006080; Defensin_mammal.
DR

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DR Pfam; PF00711; Defensin_beta; 1.
DR SMART; SM00048; DEFSN; 1.
KW Antibiotic; Cleavage on pair of basic residues; signal.
FT SIGNAL 1 20 Potential.
FT PROPEP 21 22 Potential.
FT CHAIN 23 63 Beta-defensin 3.
FT DISULFID 31 59 By similarity.
FT DISULFID 38 52 By similarity.
FT DISULFID 42 60 By similarity.
SQ SEQUENCE 63 AA; 7126 MW; 9D59EC8AD15EA330 CRC64;

Query Match
Best Local Similarity 13.8%; Score 9; DB 1; Length 63;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRLHYLLFA 9
DB 1 MRLHYLLFA 9

RESULT 7
Q9EPV9 PRELIMINARY; PRT; 64 AA.
AC Q9EPV9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Defensin beta 5.
GN Name=Defb5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Adler D.A., Holloway J.L., Haldeman B.E., Rixon M., Jaspers S.,
RA Fox B., Goshik J., Sheppard P., Presnell S., Gao Z., Whitmore T.,
RA Stamm M., Laube D., Diamond G.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF318068; AAC49340.1; -
DR MGI; MGI:1933153; Defb5.
SQ SEQUENCE 64 AA; 7087 MW; 6105153157A27B3B CRC64;

Query Match
Best Local Similarity 13.8%; Score 9; DB 2; Length 64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRLHYLLFA 9
DB 1 MRLHYLLFA 9

RESULT 8
BD01_CHILA STANDARD; PRT; 67 AA.
AC P83943;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-defensin 1 precursor (GSD-1).
GN Name=DEFB1; Synonym=BD1.
OS Chinchilla lanigera (Chinchilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Chinchillidae;
OC Chinchilla.
NCBI_Taxid=34835;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND MASS
RP SPECTROMETRY.
RC TISSUE=lung, and Trachea;
RX PubMed=14996845; DOI=10.1074/jbc.M400499200;
RA Harris R.H., Milk D., Bevins C.L., Munson R.S., Jr., Bakaletz L.O.;
RA "Identification and characterization of mucosal antimicrobial peptides

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RT expressed by the chinchilla (Chinchilla lanigera) airway.";
RL J Biol. Chem. 279:20250-20256(2004).
CC -1- FUNCTION: Has antibacterial activity against Gram-positive
CC bacterium S.pneumoniae. Serotype 14 is also active against Gram-
CC negative bacteria K.carnalis 1657, and nontypable H.influenzae
CC strains 86-028NP and 1128. Has antifungal activity against
CC C.albicans. May have a role in maintaining sterility in the middle
CC ear.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Highly expressed in tongue, nasopharyngeal
CC mucosa and skin, and to a lower extent in the Eustachian tube,
CC lung and trachea.
CC -1- MASS SPECTROMETRY: MW=5123; METHOD=Electrospray; RANGE=23-67;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the beta-defensin family.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AY128668; AAM97293.1; -
DR InterPro; IPR006080; Defensin_mammal.
DR SMART; SM00048; DEFSN; 1.
KW Antibiotic; Fungicide; Signal.
FT SIGNAL 1 22 Potential.
FT CHAIN 23 67 Beta-defensin 1.
FT DISULFID 33 62 By similarity.
FT DISULFID 40 55 By similarity.
FT DISULFID 45 62 By similarity.
SQ SEQUENCE 67 AA; 7676 MW; 30A611CCDCDB5A8D CRC64;

Query Match
Best Local Similarity 13.8%; Score 9; DB 1; Length 67;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRLHYLLFA 9
DB 1 MRLHYLLFA 9

RESULT 9
Q91V82 PRELIMINARY; PRT; 60 AA.
AC Q91V82;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Beta-defensin 8 (Beta-defensin 6).
GN Name=Defb8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RP TISSUE=Lung;
RC Conejo-Garcia J.R., Nehls M.C., Wattler S., Bais R., Heitland A.,
RA Kluever E., Lieske C., Ademann K., Forsmann W.G.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RP TISSUE=Lung;
RA Krause A.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ300674; CAC44635.1; -
DR EMBL; AJ300673; CAC44634.1; -
DR PDB; 1E4R; NMR; A=26-60.
DR MGI; MGI:2654206; Defb8.
GO; GO:0042742; P:defense response to bacteria; IDA.

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DR InterPro: IPR001855; Defensin_beta.
DR Pfam: PF00711; Defensin_beta; 1.
SQ SEQUENCE 60 AA; 6760 MW; 7213024CF909A59B CRC64;

Query Match
Best Local Similarity 12.3%; Score 8; DB 2; Length 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHIHYLF 8
Db 1 MHIHYLF 8

RESULT 10
Q8R556 PRELIMINARY; PRT; 60 AA.
ID Q8R556
AC Q8R556;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Defensin related peptide.
DE Defensin related peptide.
GN Name=Defb8; Synonyms=Defb11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J;
RX MEDLINE=22213784; PubMed=12226710;
RA Morrison G.M., Rolfe M., Kilanowski P.M., Cross S.H., Dorin J.R.;
RT "Identification and characterisation a novel murine beta defensin
related gene."
RL Mamm. Genome 13:445-451(2002).
DR EMBL: AJ34114; AAC86998.1;
DR HSSP: Q15263; 1PDB3.
DR MGD; MGI:2654206; Defb8.
DR GO; GO:0042742; P:defense response to bacteria; IDA.
DR InterPro: IPR001855; Defensin_beta.
DR Pfam; PF00711; Defensin_beta; 1.
SQ SEQUENCE 60 AA; 6820 MW; 3702A95649120351 CRC64;

Query Match
Best Local Similarity 12.3%; Score 8; DB 2; Length 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHIHYLF 8
Db 1 MHIHYLF 8

RESULT 11
BD02_RAT STANDARD; PRT; 63 AA.
ID BD02_RAT
AC O88514;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-defensin 2 precursor (BD-2) (RBD-2).
GN Name=Defb2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCB1_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=98386883; PubMed=10456937;
RA Jia H.P., Mills J.N., Barhamand-Pour F., Nishimura D.,
RA Mallampalli R.K., Wang G., Wiles K., Tack B.F., Bevins C.L.,
RA Mccrory P.B. Jr.;
RT "Molecular cloning and characterization of rat genes encoding
homologues of human beta-defensins."

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RL Infect. Immun. 67:4827-4833(1999).
CC -1- FUNCTION: Has bactericidal activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- TISSUE SPECIFICITY: Highly expressed in lung.
CC -1- SIMILARITY: Belongs to the beta-defensin family. IAP/TAP
subfamily.
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DR EMBL: AF068861; AAC28072.1; -.
DR HSSP: Q15263; 1P40.
DR RSD; 619944; Defb2.
DR InterPro: IPR001855; Defensin_beta.
DR Pfam; PF00711; Defensin_beta; 1.
DR SMART; SM00048; DEFSN; 1.
DR Anticlotic; Signal.
FT SIGNAL 1 20 Potential.
FT PROPEP 21 7 Potential.
FT CHAIN 22 63 Beta-defensin 2.
FT DISULFID 31 59 By similarity.
FT DISULFID 38 52 By similarity.
FT DISULFID 42 60 By similarity.
SQ SEQUENCE 63 AA; 6946 MW; 826099DE2144ACF4 CRC64;

Query Match
Best Local Similarity 12.3%; Score 8; DB 1; Length 63;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHIHYLF 8
Db 1 MHIHYLF 8

RESULT 12
BD04_MOUSE STANDARD; PRT; 63 AA.
ID BD04_MOUSE
AC P82019;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-defensin 4 precursor (BD-4) (mbd-4).
GN Name=Defb4; Synonyms=Bdef4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.; TISSUE SPECIFICITY, AND VARIANT PRO-12.
RC STRAIN=CS7BL/6, 129/SvJ, and FVB; TISSUE=Lung;
RX MEDLINE=20517883; PubMed=10922379;
RA Jia H.P., Mowk S.A., Schutte B.C., Lee S.K., Vivado A., Tack B.F.,
RA Bevins C.L., Mccrory P.B. Jr.;
RT "A novel murine beta-defensin expressed in tongue, esophagus, and
trachea."
RL J. Biol. Chem. 275:33314-33320(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J; TISSUE=Tongue;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nishida I., Osato N., Saito R., Suzuki H., Yamahata I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
RA Baldeirelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schiraldi L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Datta E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

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RA Gaasterland T., Gariboldi M., Gisel C., Godzik A., Gough J.,
 RA Grimmond S., Gustinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kani A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kongsaya A., Kurouchkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltas L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numa K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempé C.A., Secou M., Shimada K.,
 RA Sultana R., Takanaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilting L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavoian M., Zhu Y., Zimmer A., Carinci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Maki K., Kawai J., Nakawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imorani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
 RA Yasunishi A., Yoshino M., Waterson R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT Nature 420:563-573(2002)."
 RL 60,770 full-length cDNAs."
 CC - FUNCTION: Has bactericidal activity (By similarity).
 CC - SUPERFAMILY LOCATION: Secreted (By similarity).
 CC - TISSUE SPECIFICITY: Tongue, esophagus and trachea.
 CC - SIMILARITY: Belongs to the beta-defensin family.
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 CC -----
 DR EMBL; AF155882; AAD38852.1; -
 DR EMBL; AF287475; AAG02197.1; -
 DR EMBL; AF288371; AAG10514.1; -
 DR EMBL; AK009306; BAB26207.1; -
 DR EMBL; AK009061; BAB26051.1; -
 DR HSSP; O15263; IE4Q.
 DR MGD; MGI:1927667; Defb4.
 DR InterPro; IPR001855; Defensin_beta.
 DR InterPro; IPR006080; Defensin_mammal.
 DR Pfam; PF00711; Defensin_beta_1.
 DR SMART; SM00048; DEFSN; 1.
 KW Antidiabetic; Signal.
 FT SIGNAL 1 22 Potential.
 FT CHAIN 23 63 Beta-defensin 4.
 FT DISULFID 31 59 By similarity.
 FT DISULFID 38 52 By similarity.
 FT DISULFID 42 60 By similarity.
 FT VARIANT 12 12 L>P (in strain PVB).
 FT VARIANT 12 12 L>P (in strain PVB).
 SQ SEQUENCE 63 AA; 7129 MW; 4C7692BD589E289 CRC64;

Query Match 12.3%; Score 8; DB 1; Length 63;
 Best Local Similarity 100.0%; Pred. No. 5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRYHYLLF 8
 DB 1 MRYHYLLF 8

RESULT 13
 OTNVS PRELIMINARY; PRT; 67 AA.
 AC OTNVS
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Beta defensin 14.
 GN Name=Defb14;

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Maxwell A.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Dorin J.R.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ578468; CAB1765.2; -
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0009613; P:response to pest/pathogen/parasite; IEA.
 DR InterPro; IPR001855; Defensin_beta.
 DR Pfam; PF00711; Defensin_beta_1.
 DR SEQUENCE 67 AA; 7718 MW; EEF0D93ADF17452 CRC64;

Query Match 12.3%; Score 8; DB 2; Length 67;
 Best Local Similarity 100.0%; Pred. No. 5.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 RGRCAVTL 43
 DB 36 RGRCAVTL 43

RESULT 14
 OTNVS PRELIMINARY; PRT; 516 AA.
 AC OTNVS
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN Ordered locus names=CV0198;
 OS Chromobacterium violaceum.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Chromobacterium.
 OX NCBI_TaxId=536;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12472 / DSM 30191;
 RX MEDLINE=22882880; PubMed=14500782;
 RA Vazconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
 RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
 RA Alves-Gomes J.A., Andrade E.M., Araújo U., de Araujo M.F.F.,
 RA Astolfi-Filho S., Azevedo V., Baptista A.U., Batous L.A.M.,
 RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
 RA Bordignon J., Brigido M.M., Brito C.A., Broccoli M., Burilly H.A.,
 RA Canagaro A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
 RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chastre L.M.O.,
 RA Cerezyński-Pesa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
 RA Fantiutti F., Farias I.P., Felipe M.S.S., Ferrati L.P., Ferro J.A.,
 RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
 RA Gazzinelli R.T., Gomes E.A., Gonçalves P.R., Grangeiro T.B.,
 RA Grattapaglia D., Gristard E.C., Hanna E.S., Jardim S.N., Laurino J.,
 RA Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
 RA Madeira H.M.F., Mantio G.P., Maranhão A.O., Martins W.S.,
 RA di Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M.,
 RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
 RA Paixão R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.O., Pereira J.O.,
 RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
 RA Ramalho-Neto C.B., Reis A.M.M., Rigo L.U., Rondinelli E.,
 RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seanez H.N.,
 RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
 RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza X.R.L.,
 RA Souza R.C., Steffens W.B.R., Steindel M., Teixeira S.R., Umenyi T.,
 RA Vettore A., Wassen R., Zaha A., Simpson A.J.G.;

RT "The complete genome sequence of *Chromobacterium violaceum* reveals
 RT remarkable and exploitable bacterial adaptability."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
 DR EMBL; AE016910; AA057877.1; -
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 516 AA; 54740 MW; EA9B80966AA9ACF CRC64;

Query Match 12.3% Score 8; DB 2; Length 516;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LIFALLFL 13
 Db 410 LIFALLFL 417

RESULT 15
 YFNM_BACSU STANDARD; PRT; 51 AA.
 ID YFNM_BACSU
 AC 006472;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Hypothetical protein yfnn.
 GN Name=yfnn; OrderedLocustNames=BSU07410;
 OS *Bacillus subtilis*.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
 OX NCBI_TaxID=1423;
 RX MEDLINE=97286547; PubMed=9141694;
 RC STRAIN=AC327;
 RT "A 23.4 kb segment at the 69 degrees-70 degrees region of the *Bacillus*
 RT *subtilis* genome."
 RL Microbiology 143:1317-1320(1997).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
 RA Kunst P., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertolo M.G., Bessieres P., Bolyard A., Borchert S.,
 RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruscia C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Conterton I.F., Cummings N.J., Daniel R.A.,
 RA Denzot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Ertan K.D., Errington J., Fabre C., Ferraci E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Gilm S.V., Glaser P., Goffeau A., Golligly E.J., Grandi G.,
 RA Guisepi G., Guy B.J., Haga K., Haeich U., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hult M.F., Itaya M.,
 RA Jones L.-W., Joris B., Karamata D., Kasahara Y., Klauer-Blanchard M.,
 RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
 RA Kuno M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
 RA Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Maul C.,
 RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
 RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
 RA Park S.H., Parro V., Pohl T.M., Portetalle D., Porwollik S.,
 RA Prescott A.M., Presseau E., Pujic P., Purnelle B., Rapoport G.,
 RA Rey M., Reynolds S., Sato T., Scanlan E., Rocha E., Roche B.,
 RA Rose M., Sadate Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
 RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Seror P.,
 RA Shin B.S., Solido B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
 RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Tarpstra P.,
 RA Topmont A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
 RA Vagstad A., Viari A., Wandt R., Wedler E., Wedler H.,
 RA Weitzelberger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
 RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumbstein E.,
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*
 RT *subtilis*."
 RL Nature 390:249-256(1997).
 CC

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 CC -----
 DR EMBL; D86417; BA22328.1; -
 DR EMBL; D86418; BA220103.1; -
 DR EMBL; Z99107; CAB12560.1; -
 DR PIR; E69813; E69813.
 DR Subtilist; Bg12965; yfnn.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 51 AA; 5924 MW; 6DB6A157B1B66030 CRC64;

Query Match 10.8% Score 7; DB 1; Length 51;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 LSCLPKE 49
 Db 44 LSCLPKE 50

Search completed: October 13, 2004, 15:00:26
 Job time : 195 secs

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OM protein - protein search, using sw model

Run on: October 13, 2004, 14:51:25 ; Search time 39 seconds

(without alignments)
160.361 Million cell updates/sec

Title: US-10-272-121-2

Perfect score: 65

Sequence: 1 MRLHLLFALLFLVFPVPG.....LPKERQIGKSGTRGRKCCR 65

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

1: pfr1:
2: pfr2:
3: pfr3:
4: pfr4:

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	10.8	51	2 E69813	hypothetical prote
2	7	10.8	101	2 JQ0877	cycD2 protein prec
3	7	10.8	125	1 NFRH1	oxytocin / neuroph
4	7	10.8	173	2 S67579	probable membrane
5	7	10.8	201	2 T10017	hypothetical prote
6	7	10.8	258	2 F83307	probable permease
7	7	10.8	302	2 B81596	4-hydroxybenzoate
8	7	10.8	312	2 T08985	hypothetical prote
9	7	10.8	373	2 B90253	high-affinity nick
10	7	10.8	378	2 D70324	hypothetical prote
11	7	10.8	380	2 AG2319	hypothetical prote
12	7	10.8	405	2 P96505	probable nucellin
13	7	10.8	437	2 B83385	hypothetical prote
14	7	10.8	485	2 JQ1957	glucagon receptor
15	7	10.8	512	2 S74561	hypothetical prote
16	7	10.8	602	2 G81654	conserved hypothet
17	7	10.8	602	2 F71496	hypothetical prote
18	7	10.8	683	1 QQBEM8	gene 29 protein -
19	7	10.8	683	1 T42943	hypothetical prote
20	7	10.8	683	1 S71752	giant protein p619
21	6	9.2	30	2 I58367	gag protein - mous
22	6	9.2	49	2 S02007	proteasome I - mous
23	6	9.2	49	2 T07307	hypothetical prote
24	6	9.2	55	2 A83500	periplasmic nitrat
25	6	9.2	73	2 T03199	hypothetical prote
26	6	9.2	75	2 B81354	probable lipoprote
27	6	9.2	76	2 A28945	neurexin B precu
28	6	9.2	77	2 A86489	hypothetical prote
29	6	9.2	77	2 A72125	hypothetical prote

30	6	9.2	77	2 AH1279	hypothetical prote
31	6	9.2	77	2 AH1642	hypothetical prote
32	6	9.2	79	2 S42861	hypothetical prote
33	6	9.2	80	2 H75569	hypothetical prote
34	6	9.2	86	2 B37402	neutrophin - babo
35	6	9.2	89	2 I51423	gonadolibetin prec
36	6	9.2	93	2 T44069	hypothetical prote
37	6	9.2	102	2 T10199	hypothetical prote
38	6	9.2	103	2 C75149	hypothetical prote
39	6	9.2	104	2 S51606	NADH dehydrogenas
40	6	9.2	105	2 F72614	hypothetical prote
41	6	9.2	113	2 S66967	probable membrane
42	6	9.2	118	2 P90459	hypothetical prote
43	6	9.2	121	2 D97087	hypothetical prote
44	6	9.2	124	2 G75416	hypothetical prote
45	6	9.2	128	2 S26430	hypothetical 14.5K

ALIGNMENTS

RESULT 1
E69813
hypothetical protein yfM - Bacillus subtilis
C/Species: Bacillus subtilis
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: E69813
R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A/Authors: Foulger, D.; Fritze, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
lechi, U.; Harwood, C.R.; Henauf, A.; Hilbert, H.; Holappel, S.; Hosono, S.; Hullo, M.F
Koelter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A/Authors: Lauber, U.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli
Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon
A/Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Sero
Akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
A/Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A/Reference number: A69580; MUID: 98044033; PMID: 9384377
A/Accession: E69813
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-51 <KUN>
A/Cross-references: UNIPROT:O06472; GB:299107; GB:299108; GB:AL009126; NID:g2633055; PI
A/Experimental source: strain 168
C/Genetics:
A/Gene: yfM
Query Match 10.8%; Score 7; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 43 LSCDPKE 49
DB 44 LSCDPKE 50
RESULT 2
JQ0877
cycD2 protein precursor - Madagascar periwinkle
C/Species: Catharanthus roseus (Madagascar periwinkle)
C/Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C/Accession: JQ0877
R/Kodama, H.; Ito, M.; Hattori, T.; Nakamura, K.; Komamine, A.
Submitted to JIPID, February 1991
A/Description: Isolation of genes that are preferentially expressed at the G1/S bounds
A/Reference number: JQ0877
A/Accession: JQ0877
A/Molecule type: mRNA

A/Residues: 1-101 <KOD>
 A/Cross-references: UNIPROT:P25923
 A/Experimental source: strain B, cell suspension culture
 C/Genetics:
 A/Gene: cyo2
 F/1-23/Domain: signal sequence #status predicted <SIG>
 F/24-101/Product: cyo2 protein #status predicted <MAT>

Query Match 10.8%; Score 7; DB 2; Length 101;
 Best Local Similarity 100.0%; Pred. No. 6.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 LFLALFL 12
 |||||
 Db 9 LFLALFL 15

RESULT 3
 NEHL
 oxytocin / neuropeptide precursor [validated] - human
 N/Alternate names: neuropeptide I; prepro-OT-NPI
 N/Contains: neuropeptide I; oxytocin
 C/Species: Homo sapiens (man)
 C/Date: 24-Apr-1984 #sequence revision 30-Sep-1987 #text change 09-Jul-2004
 C/Accession: A94676; A91352; A93948; A91292; A37402; I84607; A01440; A01450; B23
 R/Sausville, E.; Carney, D.; Bartley, J.
 J. Biol. Chem. 260, 10236-10241, 1985
 A/Title: The human vasopressin gene is linked to the oxytocin gene and is selectively ex
 A/Reference number: A94676; UID:85261445; PMID:2991279
 A/Accession: A94676
 A/Molecule type: DNA
 A/Residues: 1-99,101-125 <SAN>
 A/Cross-references: UNIPROT:P01178; GB:M1186; NID:9189414; PID:AAA8806.1; PID:9386994
 R/Mohr, E.; Hillier, M.; Ivell, R.; Haulica, I.D.; Richter, D.
 FEBS Lett. 193, 12-16, 1985
 A/Title: Expression of the vasopressin and oxytocin genes in human hypothalam.
 A/Reference number: A91352; UID:86056283; PMID:4065330
 A/Accession: A91352
 A/Molecule type: mRNA
 A/Residues: 80-125 <MOH>
 A/Cross-references: GB:X03173; NID:935170; PID:GMA26936.1; PID:9825699
 R/Light, A.; du Vigneaud, V.
 Proc. Soc. Exp. Biol. Med. 98, 692-696, 1958
 A/Title: On the nature of oxytocin and vasopressin from human pituitary.
 A/Reference number: A94229
 A/Accession: A94229
 A/Molecule type: protein
 A/Residues: 20-28 <LIG>
 R/Chavet, M.T.; Hurp, D.; Chavet, J.; Acher, R.
 Proc. Natl. Acad. Sci. U.S.A. 80, 2839-2843, 1983
 A/Title: Identification of human neuropeptides: complete amino acid sequences of MSL- an
 A/Reference number: A93948; UID:83221497; PMID:6574452
 A/Accession: A93948
 A/Molecule type: protein
 A/Residues: 32-125 <CH>
 R/Schlesinger, D.H.; Audy, T.K.
 FEBS Lett. 128, 325-328, 1981
 A/Title: A comparative study of mammalian neuropeptide protein sequences.
 A/Reference number: A91292; UID:81261248; PMID:7262323
 A/Accession: A91292
 A/Molecule type: protein
 A/Residues: 32-99,AA',102-123,'L',125 <SCH>
 R/Ivell, R.; Futaya, K.; Brackmann, B.; Dawood, Y.; Khan-Dawood, F.
 Endocrinology 127, 2990-2996, 1990
 A/Title: Expression of the oxytocin and vasopressin genes in human and baboon gonadal ti
 A/Reference number: A37402; UID:91065270; PMID:2249637
 A/Accession: A37402
 A/Molecule type: mRNA
 A/Residues: 25-99,'G',95-110 <IVE>
 A/Cross-references: GB:M62611; NID:9189416; PID:AAA59979.1; PID:9189417
 R/Rehbein, M.; Hillier, M.; Mohr, E.; Ivell, R.; Morley, S.; Schmale, H.; Richter, D.
 Biol. Chem. Hoppe-Seyler 367, 695-704, 1986
 A/Title: The neurohypophyseal hormones vasopressin and oxytocin. Precursor structure, sy

A/Reference number: I45952; UID:87026235; PMID:3768139
 A/Accession: I84607
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-125 <RES>
 A/Cross-references: GB:M2650; NID:9189410; PID:AAA59977.1; PID:9189411
 C/Genetics:
 A/Gene: GDB:OXT; OT
 A/Cross-references: GDB:120253; OMIM:167050
 A/Map position: 20p13-20p13
 A/Introns: 40/3; 108/1
 C/Function:
 A/Description: oxytocin is a posterior pituitary peptide hormone that induces uterine c
 oxytocin
 C/Superfamily: oxytocin-neuropeptide
 C/Keywords: amidated carboxyl end; hormone; lactation; posterior pituitary
 F/1-19/Domain: signal sequence #status predicted <SIG>
 F/20-28/Product: oxytocin #status experimental <OXN>
 F/32-125/Product: neuropeptide I #status experimental <NPI>
 F/20-25/Disulfide bonds: #status experimental
 F/28/Modified site: amidated carboxyl end (Gly) (amide in mature form from following gly
 F/41-85,44-58,52-75,59-65,92-104,98-116,105-110/Disulfide bonds: #status predicted

Query Match 10.8%; Score 7; DB 1; Length 125;
 Best Local Similarity 100.0%; Pred. No. 7.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 37 GGRCAVLT 43
 |||||
 Db 95 GGRCAVLT 101

RESULT 4
 S67579
 probable membrane protein YDLO46w - Yeast (Saccharomyces cerevisiae)
 N/Alternate names: hypothetical protein D2699
 C/Species: Saccharomyces cerevisiae
 C/Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text change 09-Jul-2004
 C/Accession: S67579
 R/Paulin, L.; Saren, A.M.; Laamanen, P.
 submitted to the Protein Sequence Database, July 1996
 A/Reference number: S67560
 A/Accession: S67579
 A/Molecule type: DNA
 A/Residues: 1-173 <PAU>
 A/Cross-references: UNIPROT:Q12408; EMBL:Z74094; NID:91431035; PID:e253204; PID:9143103
 A/Experimental source: strain S288C
 C/Genetics:
 A/Gene: MIPS:YDLO46w
 A/Cross-references: SGD:S0002204
 A/Map position: 4L
 C/Superfamily: Saccharomyces cerevisiae probable membrane protein YDLO46w
 C/Keywords: transmembrane protein
 F/8-24/Domain: transmembrane #status predicted <TM>

Query Match 10.8%; Score 7; DB 2; Length 173;
 Best Local Similarity 100.0%; Pred. No. 9.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 LFLALFL 13
 |||||
 Db 8 LFLALFL 14

RESULT 5
 T10017
 hypothetical protein - Mycobacterium leprae
 C/Species: Mycobacterium leprae
 C/Date: 16-Jul-1999 #sequence revision 16-Jul-1999 #text change 09-Jul-2004
 C/Accession: T10017
 R/Cole, S.T.
 submitted to the EMBL Data Library, August 1997
 A/Reference number: Z16916

A/Accession: T10017
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-201 <COL>
 A/Cross-references: UNIPROT:Q9CDE0; EMBL:270722; NID:e1059634; PID:e338507
 C/Genetics:
 A/Note: MBL1770.17c

Query Match 10.8%; Score 7; DB 2; Length 201;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LFLFLVP 17
 Db 75 LFLFLVP 81

RESULT 6

P33207
 probable peptidase of ABC transporter PA3512 [imported] - Pseudomonas aeruginosa (strain
 C/Species: Pseudomonas aeruginosa
 C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C/Accession: F83207

R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Braham, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim, J.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A/Reference number: A82950; MUID:20437337; PMID:10984043

A/Accession: F83207

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-258 <STO>

A/Cross-references: UNIPROT:Q9HY97; GB:AE004771; GB:AE004091; NID:g9949650; PIDN:AA0690

A/Experimental source: strain PA01

C/Genetics:

A/Gene: PA3512

C/Superfamily: Synecococcus nitrate transport protein nrtB

Query Match 10.8%; Score 7; DB 2; Length 258;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ALLFLFL 15
 Db 13 ALLFLFL 19

RESULT 7

B81696
 4-hydroxybenzoate octaprenyltransferase TC0492 [imported] - Chlamydia muridarum (strain
 C/Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
 C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C/Accession: B81696

R/Read, T.D.; Brumham, R.C.; Sheu, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gaim, M.; Nelson, M.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000

A/Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
 A/Reference number: A81500; MUID:20150255; PMID:10684935

A/Accession: B81696

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-302 <RET>

A/Cross-references: UNIPROT:Q9PKX3; GB:AE002318; GB:AE002160; NID:g7190531; PIDN:AAF3933

C/Genetics:

A/Gene: TC0492

C/Superfamily: 4-hydroxybenzoate octaprenyltransferase

Query Match 10.8%; Score 7; DB 2; Length 302;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LFLFLFL 13
 Db 17 LFLFLFL 23

RESULT 8

T08985
 hypothetical protein F6G3.120 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C/Accession: T08985

R/Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F. submitted to the Protein Sequence Database, May 1999

A/Reference number: Z16520

A/Accession: T08985

A/Molecule type: DNA

A/Residues: 1-312 <BEV>

A/Cross-references: UNIPROT:Q9SZW2; EMBL:AL078464; GSPDB:GN00062; ATSP:F6G3.120

A/Experimental source: cultivar Columbia; BAC clone F6G3

C/Genetics:

A/Gene: ATSP:F6G3.120

A/Map position: 4
 A/Intons: 55/1; 94/3; 115/3; 151/3; 168/3; 189/3; 241/3; 264/3; 285/2

Query Match 10.8%; Score 7; DB 2; Length 312;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LFLFLFLV 16
 Db 7 LFLFLFLV 13

RESULT 9

B90253

high-affinity nickel-transport protein (hoxN) hoxN [imported] - Sulfolobus solfataricus

C/Species: Sulfolobus solfataricus

C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C/Accession: B90253

R/She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweez, M.S.; Chan Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.

submitted to Genbank, April 2001

A/Description: Sulfolobus solfataricus complete genome.

A/Reference number: A99139

A/Accession: B90253

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-373 <KUR>

A/Cross-references: UNIPROT:Q97ZB2; GB:AE006641; NID:g13814199; PIDN:AAK41281.1; GSPDB:

C/Genetics:

A/Gene: hoxN

C/Superfamily: nickel transport protein YPO2673

Query Match 10.8%; Score 7; DB 2; Length 373;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ALLFLFL 15
 Db 50 ALLFLFL 56

RESULT 10

D70324
 hypothetical protein aq_267 - Aquifex aeolicus

C/Species: Aquifex aeolicus

C/Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C/Accession: D70324

R/Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; C

V. Nature 392, 353-358, 1998

A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

```

A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: D70324
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-578 <AGT>
A:Cross-references: UNIPROT:O66624; GB:AE000661; NID:92989263; PIDs:AA06585.1; PID:92989263
A:Experimental source: strain VPS
C:Genetics:
A:Gene: aq_267

Query Match 10.8%; Score 7; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LFAFLFL 13
|||||
Db 247 LFAFLFL 253

RESULT 11
AG2319
hypothetical protein al14110 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Ncnc: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kurita, T.; Saemoto, S.; Matsumoto, A.; Iriguchi, S.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takasawa, M.; Yamada, M.; Yasuda, M.; Tadate, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG2319
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-380 <KUR>
A:Cross-references: UNIPROT:O8YET1; GB:BA000019; PIDs:BA075809.1; PID:G17133245; GSPDB:G:G17133245
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: al14110
C:Superfamily: magnesium and cobalt transport protein

Query Match 10.8%; Score 7; DB 2; Length 380;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 FALFLFL 14
|||||
Db 359 FALFLFL 365

RESULT 12
P96505
probable nucleolin [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
A:Accession: P96505
R:Theologis, A.; Ecker, J.R.; Palm, C.U.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.;
Chen, C.W.; Chung, M.K.; Comai, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hultine, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salberg, S.L.; Schwartz, D.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: P96505
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-405 <STO>
A:Cross-references: UNIPROT:O9CGY5; GB:AE005173; NID:G11120822; PIDs:AA031001.1; GSPDB:G:G11120822
C:Genetics:

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A:Gene: T7023.17
 A:Map position: 1

Query Match	10.8%; Score 7; DB 2; Length 405;
Best Local Similarity 100.0%; Pred. No. 18;	
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	10 L L F F L V 16
Db	8 L L F F L V 14

RESULT 13
 E83385
 Hypothetical protein PA2091 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C:Accession: E83385
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapidis, K.; Lim
 , J.; Jory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: E83385
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-427 <SNO>
 A:Cross-references: UNIPROT:Q91224; GB:AE004636; GB:AE004091; NID:g9948093; PIDN:AA054
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA2091
 C:Superfamily: hypothetical protein c0103

Query Match	10.8%; Score 7; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 19;	
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	5 Y L F A L L 11
Db	122 Y L F A L L 128

RESULT 14
 J01957
 glucagon receptor - rat
 N:Alternate names: GLP-1 receptor homolog, hepatic
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C:Accession: J01957; A46211; S29688
 R:Stoboda, M.; Ciccarelli, E.; Tasenay, M.; Gavril, A.; Stievenart, M.; Christophe, J
 Biochem. Biophys. Res. Commun. 191, 479-486, 1993
 A:Title: Small introns in a hepatic cDNA encoding a new glucagon-like peptide 1-type re
 A:Reference number: J01957; MUID:93213282; PMID:8384842
 A:Accession: J01957
 A:Molecule type: mRNA
 A:Residues: 1-485 <SVO>
 A:Cross-references: UNIPROT:P30082; GB:X68692
 A:Experimental source: liver
 R:Jeinek, L.U.; Lok, S.; Rosenberg, G.B.; Smith, R.A.; Grant, F.J.; Biggs, S.; Bensch,
 rnan, P.A.; Kindsvogel, W.
 Science 259, 1614-1616, 1993
 A:Title: Expression cloning and signaling properties of the rat glucagon receptor.
 A:Reference number: A46211; MUID:93206096; PMID:8384375
 A:Accession: A46211
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr
 A:Molecule type: mRNA
 A:Residues: 1-37, 'W', '38-215', 'W', '217-323', 'V', '325-485
 A:Experimental source: liver
 A:Note: sequence extracted from NCB1 backbone (NCBIF:127785)
 C:Genetics:
 A:Introns: 132/3; 168/2; 220/3; 407/3
 C:Superfamily: glucagon receptor

C:Keywords: G protein-coupled receptor; glycoprotein; liver; phosphoprotein; transmembrane
 F:114-157/Domain: transmembrane #status predicted <TM1>
 F:175-184/Domain: transmembrane #status predicted <TM2>
 F:127-251/Domain: transmembrane #status predicted <TM3>
 F:264-286/Domain: transmembrane #status predicted <TM4>
 F:305-324/Domain: transmembrane #status predicted <TM5>
 F:352-370/Domain: transmembrane #status predicted <TM6>
 F:389-405/Domain: transmembrane #status predicted <TM7>
 F:47-60,75,79/Binding site: carbohydrate (asn) (covalent) #status predicted
 F:432/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 10.8%; Score 7; DB 2; Length 485;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VLSCLPK 48
 |||||
 DB 17 VLSCLPK 23

RESULT 15

S74561
 hypothetical protein sl10225 - Synechocystis sp. (strain PCC 6803)

C:Species: Synechocystis sp.

A:Variate: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: S74561

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-116, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

S.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S74561

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-512 <KAN>

A:CROSS-references: UNIPROT:P72706; EMBL:D90900; GB:AE01339; NID:G1651768; PIDN:BA11671

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Genetics:

A:Start codon: GTG

Query Match 10.8%; Score 7; DB 2; Length 512;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FLVPVPG 20
 |||||
 DB 424 FLVPVPG 430

Search completed: October 13, 2004, 15:01:12
 Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 14:54:25 ; Search time 129 Seconds

(without alignments)
162.592 Million cell updates/sec

Title: US-10-272-121-2

Perfect score: 65
Sequence: 1 MRHYLLFALLFLVPEVPG.....LPKEBQIGKSTRGKCCR 65

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 135658 seqs, 322682953 residues

Word size : 0

Total number of hits satisfying chosen parameters: 135658

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	100.0	65	14	US-10-091-166B-2
2	65	100.0	65	14	US-10-272-121-2
3	65	100.0	65	14	US-10-409-366-2
4	65	100.0	65	14	US-10-409-352-2
5	65	100.0	67	9	US-09-917-340-52
6	65	100.0	67	9	US-09-917-340-72
7	65	100.0	67	9	US-09-872-852-2
8	65	100.0	67	14	US-10-091-166B-10
9	65	100.0	67	14	US-10-272-121-10
10	65	100.0	67	14	US-10-409-366-10
11	65	100.0	67	14	US-10-409-352-10
12	43	66.2	45	9	US-09-872-852-4
13	42	64.6	44	16	US-10-332-765-27
14	39	60.0	41	9	US-09-872-852-3

15	35	53.8	35	14	US-10-252-734-7	Sequence 7, Appli
16	31	47.7	31	16	US-10-332-765-1	Sequence 1, Appli
17	20	30.8	36	14	US-10-091-166B-60	Sequence 60, Appli
18	20	30.8	36	14	US-10-272-121-60	Sequence 60, Appli
19	20	30.8	36	14	US-10-409-366-60	Sequence 60, Appli
20	20	30.8	36	14	US-10-409-352-60	Sequence 60, Appli
21	20	30.8	37	14	US-10-091-166B-58	Sequence 58, Appli
22	20	30.8	37	14	US-10-091-166B-59	Sequence 58, Appli
23	20	30.8	37	14	US-10-272-121-58	Sequence 58, Appli
24	20	30.8	37	14	US-10-272-121-59	Sequence 58, Appli
25	20	30.8	37	14	US-10-409-366-58	Sequence 58, Appli
26	20	30.8	37	14	US-10-409-366-59	Sequence 58, Appli
27	20	30.8	37	14	US-10-409-352-58	Sequence 58, Appli
28	20	30.8	37	14	US-10-409-352-59	Sequence 58, Appli
29	20	30.8	38	14	US-10-091-166B-56	Sequence 56, Appli
30	20	30.8	38	14	US-10-091-166B-57	Sequence 56, Appli
31	20	30.8	38	14	US-10-272-121-56	Sequence 56, Appli
32	20	30.8	38	14	US-10-272-121-57	Sequence 56, Appli
33	20	30.8	38	14	US-10-409-366-56	Sequence 56, Appli
34	20	30.8	38	14	US-10-409-366-57	Sequence 56, Appli
35	20	30.8	38	14	US-10-409-352-56	Sequence 56, Appli
36	20	30.8	38	14	US-10-409-352-57	Sequence 56, Appli
37	20	30.8	39	14	US-10-091-166B-54	Sequence 54, Appli
38	20	30.8	39	14	US-10-091-166B-55	Sequence 54, Appli
39	20	30.8	39	14	US-10-272-121-54	Sequence 54, Appli
40	20	30.8	39	14	US-10-272-121-55	Sequence 54, Appli
41	20	30.8	39	14	US-10-409-366-54	Sequence 54, Appli
42	20	30.8	39	14	US-10-409-366-55	Sequence 54, Appli
43	20	30.8	39	14	US-10-409-352-54	Sequence 54, Appli
44	20	30.8	39	14	US-10-409-352-55	Sequence 54, Appli
45	20	30.8	40	14	US-10-091-166B-52	Sequence 52, Appli

ALIGNMENTS

RESULT 1
US-10-091-166B-2
; Sequence 2, Application US/10091166B
; Publication No. US20030143671A1
GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baidur, Nand
; APPLICANT: Baisel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEPENSINS
; FILE REFERENCE: 97-44D1
; CURRENT APPLICATION NUMBER: US/10/091,166B
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/636,399
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 09/344,097
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: US 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/058,335
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-091-166B-2

Query Match 100.0%; Score 65; DB 14; Length 65;
Best Local Similarity 100.0%; Pred. No. 8.3e-59;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 MRHYLLFALLFLVPEVPGHGIINTLQKYCYRVRGRCAYVSCLPKEBQIGKSTRGR 60

Patent No. US20020090369A1
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McNulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/290,932
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 52
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-09-917-340-52

Query Match 100.0%; Score 65; DB 9; Length 67;
Best Local Similarity 100.0%; Pred. No. 8.5e-59;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MRIHYLLFALLFLVLPVPGHGIINTLOKYYCVRGRCVAVLSCLPKEBOIGKSTRGR 60

QY 61 KCCRR 65
DB 61 KCCRR 65

RESULT 6

US-09-917-340-72
Sequence 72, Application US/09917340
Patent No. US20020090369A1
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McNulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/290,932
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 72
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-09-917-340-72

Query Match 100.0%; Score 65; DB 9; Length 67;
Best Local Similarity 100.0%; Pred. No. 8.5e-59;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MRIHYLLFALLFLVLPVPGHGIINTLOKYYCVRGRCVAVLSCLPKEBOIGKSTRGR 60

QY 61 KCCRR 65
DB 61 KCCRR 65

RESULT 7
US-09-872-852-2
Sequence 2, Application US/09872852
Patent No. US20020115602A1
GENERAL INFORMATION:
APPLICANT: MCCRAY JR, PAUL B.
APPLICANT: TACK, BRIAN
APPLICANT: JIA, HONG PENG
APPLICANT: SCHUTTE, BRIAN C.
TITLE OF INVENTION: HUMAN BETA-DEFENSIN-3 (HBD-3), A HIGHLY CATIONIC
FILE REFERENCE: IOWA:031US
CURRENT APPLICATION NUMBER: US/09/872,852
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 60/208,792
PRIOR FILING DATE: 2000-06-01
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 67
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-09-872-852-2

Query Match 100.0%; Score 65; DB 9; Length 67;
Best Local Similarity 100.0%; Pred. No. 8.5e-59;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLVLPVPGHGIINTLOKYYCVRGRCVAVLSCLPKEBOIGKSTRGR 60
DB 1 MRIHYLLFALLFLVLPVPGHGIINTLOKYYCVRGRCVAVLSCLPKEBOIGKSTRGR 60

QY 61 KCCRR 65
DB 61 KCCRR 65

RESULT 8

US-10-091-166B-10
Sequence 10, Application US/10091166B
Publication No. US20030143671A1
GENERAL INFORMATION:
APPLICANT: Adler, David A.
APPLICANT: Holloway, James L.
APPLICANT: Baidur, Nand
APPLICANT: Beigel-Orme, Stephanie
APPLICANT: Shepard, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44DI
CURRENT APPLICATION NUMBER: US/10/091,166B
CURRENT FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 09/636,399
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: US 09/344,097
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: US 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: US 60/058,335
PRIOR FILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: fastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-10-091-166B-10

Query Match 100.0%; Score 65; DB 14; Length 67;
Best Local Similarity 100.0%; Pred. No. 8.5e-59;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHIHYLFLFLFVLPVPGHGIINTLQKYYCRVGRCAVLSCLPKKEQIGKSTRGR 60
DB 1 MHIHYLFLFLFVLPVPGHGIINTLQKYYCRVGRCAVLSCLPKKEQIGKSTRGR 60

QY 61 KCCR 65
DB 61 KCCR 65

RESULT 9
US-10-272-121-10
Sequence 10, Application US/10272121
Publication No. US20030157638A1
GENERAL INFORMATION:
APPLICANT: Adler, David A.
APPLICANT: Hollaway, James L.
APPLICANT: Baidur, Nand
APPLICANT: Beigel-Orme, Stephanie
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44D2
CURRENT APPLICATION NUMBER: US/10/272,121
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 09/636,399
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: US 09/344,097
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: US 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: US 60/058,335
PRIOR FILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-10-272-121-10

Query Match 100.0%; Score 65; DB 14; Length 67;
Best Local Similarity 100.0%; Pred. No. 8.5e-59;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHIHYLFLFLFVLPVPGHGIINTLQKYYCRVGRCAVLSCLPKKEQIGKSTRGR 60
DB 1 MHIHYLFLFLFVLPVPGHGIINTLQKYYCRVGRCAVLSCLPKKEQIGKSTRGR 60

QY 61 KCCR 65
DB 61 KCCR 65

RESULT 10
US-10-409-366-10
Sequence 10, Application US/10409366
Publication No. US20030166912A1
GENERAL INFORMATION:
APPLICANT: Adler, David A.
APPLICANT: Hollaway, James L.
APPLICANT: Baidur, Nand
APPLICANT: Beigel-Orme, Stephanie
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT APPLICATION NUMBER: US/10/409,366
CURRENT FILING DATE: 2003-04-07

PRIOR APPLICATION NUMBER: US/09/636,399A
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/058,335
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/636,399
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-10-409-366-10

Query Match 100.0%; Score 65; DB 14; Length 67;
Best Local Similarity 100.0%; Pred. No. 8.5e-59;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MHIHYLFLFLFVLPVPGHGIINTLQKYYCRVGRCAVLSCLPKKEQIGKSTRGR 60

QY 61 KCCR 65
DB 61 KCCR 65

RESULT 11
US-10-409-532-10
Sequence 10, Application US/10409532
Publication No. US20030166913A1
GENERAL INFORMATION:
APPLICANT: Adler, David A.
APPLICANT: Hollaway, James L.
APPLICANT: Baidur, Nand
APPLICANT: Beigel-Orme, Stephanie
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT APPLICATION NUMBER: US/10/409,532
CURRENT FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: US/09/636,399A
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/058,335
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/636,399
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-10-409-532-10

Query Match 100.0%; Score 65; DB 14; Length 67;
Best Local Similarity 100.0%; Pred. No. 8.5e-59;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MHIHYLFLFLFVLPVPGHGIINTLQKYYCRVGRCAVLSCLPKKEQIGKSTRGR 60

QY 61 KCCR 65
DB 61 KCCR 65

Db 61 KCCR 65

RESULT 12
US-09-872-852-4
; Sequence 4, Application US/09872852
; Patent No. US20020115602A1
; GENERAL INFORMATION:
; APPLICANT: MCCRAY JR, PAUL B.
; APPLICANT: TACK, BRIAN
; APPLICANT: JIA, HONG PENG
; APPLICANT: SCHUTTE, BRIAN C.
; TITLE OF INVENTION: HUMAN BETA-DEFENSIN-3 (HBD-3), A HIGHLY CATIONIC
; FILE REFERENCE: IOMA:031US
; CURRENT APPLICATION NUMBER: US/09/872,852
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/208,792
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-872-852-4

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Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GIINTLQKYYCRVGRGCAVLSCLPKKEQIGKSTRGRKCCR 43

RESULT 13
US-10-332-765-27
; Sequence 27, Application US/10332765
; Publication No. US20040116652A1
; GENERAL INFORMATION:
; APPLICANT: Forsemann, Wolf-Georg
; APPLICANT: Conejo-Garcia, Jose-Ramon
; APPLICANT: Adermann, Knut
; TITLE OF INVENTION: Method for Producing and Using Novel Human Defensins as Biologics
; FILE REFERENCE: 022584US
; CURRENT APPLICATION NUMBER: US/10/332,765
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: DE10033505.5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 27
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-332-765-27

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Best Local Similarity 100.0%; Pred. No. 2.1e-35;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 IINTLQKYYCRVGRGCAVLSCLPKKEQIGKSTRGRKCCR 42

RESULT 14
US-09-872-852-3

; Sequence 3, Application US/09872852
; Patent No. US20020115602A1
; GENERAL INFORMATION:
; APPLICANT: MCCRAY JR, PAUL B.
; APPLICANT: TACK, BRIAN
; APPLICANT: JIA, HONG PENG
; APPLICANT: SCHUTTE, BRIAN C.
; TITLE OF INVENTION: HUMAN BETA-DEFENSIN-3 (HBD-3), A HIGHLY CATIONIC
; FILE REFERENCE: IOMA:031US
; CURRENT APPLICATION NUMBER: US/09/872,852
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/208,792
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-872-852-3

Query Match 60.0%; Score 39; DB 9; Length 41;
Best Local Similarity 100.0%; Pred. No. 2.3e-32;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TLQKYYCRVGRGCAVLSCLPKKEQIGKSTRGRKCCR 65
Db 1 TLQKYYCRVGRGCAVLSCLPKKEQIGKSTRGRKCCR 39

RESULT 15
US-10-252-734-7
; Sequence 7, Application US/10252734
; Publication No. US2003017652A1
; GENERAL INFORMATION:
; APPLICANT: MCCRAY, JR., PAUL B.
; APPLICANT: SCHUTTE, BRIAN C.
; APPLICANT: JIA, HONG PENG
; APPLICANT: CASAVANT, THOMAS L.
; TITLE OF INVENTION: HUMAN AND MOUSE B-DEFENSIN, ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: IOMA:041US
; CURRENT APPLICATION NUMBER: US/10/252,734
; PRIOR FILING DATE: 2002-09-23
; CURRENT APPLICATION NUMBER: 60/323,991
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-252-734-7

Query Match 53.8%; Score 35; DB 14; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.5e-28;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 YYCRVGRGCAVLSCLPKKEQIGKSTRGRKCCR 65
Db 1 YYCRVGRGCAVLSCLPKKEQIGKSTRGRKCCR 35

Search completed: October 13, 2004, 15:04:09
Job time : 130 secs

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OM protein - protein search, using sw model

Run on: October 13, 2004, 14:52:15 ; Search time 38 Seconds
(without alignments)
113.439 Million cell updates/sec

Title: US-10-272-121-2

Perfect score: 65
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Gapop 60.0, Gapext 60.0

Searched: 478139 seqs, 66318000 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database: Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	100.0	65	4 US-09-636-399A-2	Sequence 2, Appl
2	65	100.0	67	4 US-09-636-399A-10	Sequence 10, Appl
3	65	100.0	67	4 US-09-917-340-52	Sequence 52, Appl
4	65	100.0	67	4 US-09-917-340-72	Sequence 72, Appl
5	65	100.0	67	4 US-09-917-340-72	Sequence 72, Appl
6	65	100.0	67	4 US-09-917-340-72	Sequence 72, Appl
7	65	100.0	67	4 US-09-917-340-72	Sequence 72, Appl
8	65	100.0	67	4 US-09-917-340-72	Sequence 72, Appl
9	65	100.0	67	4 US-09-917-340-72	Sequence 72, Appl
10	65	100.0	67	4 US-09-917-340-72	Sequence 72, Appl
11	65	100.0	67	4 US-09-917-340-72	Sequence 72, Appl
12	65	100.0	67	4 US-09-917-340-72	Sequence 72, Appl
13	65	100.0	67	4 US-09-917-340-72	Sequence 72, Appl
14	65	100.0	67	4 US-09-917-340-72	Sequence 72, Appl
15	65	100.0	67	4 US-09-917-340-72	Sequence 72, Appl
16	65	100.0	67	4 US-09-917-340-72	Sequence 72, Appl
17	65	100.0	67	4 US-09-917-340-72	Sequence 72, Appl
18	65	100.0	67	4 US-09-917-340-72	Sequence 72, Appl
19	65	100.0	67	4 US-09-917-340-72	Sequence 72, Appl
20	65	100.0	67	4 US-09-917-340-72	Sequence 72, Appl
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22	65	100.0	67	4 US-09-917-340-72	Sequence 72, Appl
23	65	100.0	67	4 US-09-917-340-72	Sequence 72, Appl
24	65	100.0	67	4 US-09-917-340-72	Sequence 72, Appl
25	65	100.0	67	4 US-09-917-340-72	Sequence 72, Appl
26	65	100.0	67	4 US-09-917-340-72	Sequence 72, Appl
27	65	100.0	67	4 US-09-917-340-72	Sequence 72, Appl

28	20	30.8	48	4 US-09-636-399A-36	Sequence 36, Appl
29	20	30.8	48	4 US-09-636-399A-37	Sequence 37, Appl
30	20	30.8	49	4 US-09-636-399A-35	Sequence 35, Appl
31	19	29.2	35	4 US-09-636-399A-62	Sequence 62, Appl
32	19	29.2	36	4 US-09-636-399A-61	Sequence 61, Appl
33	18	27.7	34	4 US-09-636-399A-64	Sequence 64, Appl
34	18	27.7	35	4 US-09-636-399A-63	Sequence 63, Appl
35	17	26.2	33	4 US-09-636-399A-66	Sequence 66, Appl
36	17	26.2	34	4 US-09-636-399A-65	Sequence 65, Appl
37	16	24.6	32	4 US-09-636-399A-68	Sequence 68, Appl
38	16	24.6	33	4 US-09-636-399A-67	Sequence 67, Appl
39	15	23.1	31	4 US-09-636-399A-70	Sequence 70, Appl
40	15	23.1	32	4 US-09-636-399A-69	Sequence 69, Appl
41	14	21.5	30	4 US-09-636-399A-72	Sequence 72, Appl
42	14	21.5	31	4 US-09-636-399A-71	Sequence 71, Appl
43	14	21.5	37	4 US-09-636-399A-14	Sequence 14, Appl
44	14	21.5	38	4 US-09-636-399A-16	Sequence 16, Appl
45	14	21.5	39	4 US-09-636-399A-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-09-636-399A-2
; Sequence 2, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Bajndur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O
; TITLE OF INVENTION: NOVEL BETA-DEPENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PaetSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-636-399A-2
Query Match 100.0%; Score 65; DB 4; Length 65;
Best Local Similarity 100.0%; Pred. No. 2.9e-63; Indels 0; Gaps 0;
Matches 65; Conservative 0; Mismatches 0;
QY 1 MRLHLLFALLFLVPPVPGHGINTLQKYYCRVRGRCAYLSCLPREDIGKSTRGR 60
DB 1 MRLHLLFALLFLVPPVPGHGINTLQKYYCRVRGRCAYLSCLPREDIGKSTRGR 60
QY 61 KCCR 65
DB 61 KCCR 65
RESULT 2
US-09-636-399A-10
; Sequence 10, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.

```
APPLICANT: Baindur, Nand
APPLICANT: Beigel-Orme, Stephanie
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT APPLICATION NUMBER: US/09/636,399A
CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/058,335
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/636,399
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-09-636-399A-10

Query Match
Best Local Similarity 100.0%; Score 65; DB 4; Length 67;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-09-917-340-52
Sequence 52, Application US/09917340
Patent No. 6696238
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/290,932
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 52
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-09-917-340-52

Query Match
Best Local Similarity 100.0%; Score 65; DB 4; Length 67;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-09-917-340-72
Sequence 72, Application US/09917340
Patent No. 6696238
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/290,932
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 72
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-09-917-340-72

Query Match
Best Local Similarity 100.0%; Score 65; DB 4; Length 67;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
US-09-636-399A-60
Sequence 60, Application US/09636399A
Patent No. 6576755
GENERAL INFORMATION:
APPLICANT: Adler, David A.
APPLICANT: Holloway, James L.
APPLICANT: Baindur, Nand
APPLICANT: Beigel-Orme, Stephanie
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT APPLICATION NUMBER: US/09/636,399A
CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/058,335
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/636,399
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Defensin polypeptide
NAME/KEY: VARIANT
LOCATION: (33)...(33)
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APPLICANT: Baindur, Nand
APPLICANT: Beigel-Orme, Stephanie
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT APPLICATION NUMBER: US/09/636,399A
CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/058,335
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/636,399
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-09-636-399A-10

Query Match
Best Local Similarity 100.0%; Score 65; DB 4; Length 67;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-09-917-340-52
Sequence 52, Application US/09917340
Patent No. 6696238
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/290,932
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 52
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-09-917-340-52

Query Match
Best Local Similarity 100.0%; Score 65; DB 4; Length 67;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-09-917-340-72
Sequence 72, Application US/09917340
Patent No. 6696238
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/290,932
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 72
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-09-917-340-72

Query Match
Best Local Similarity 100.0%; Score 65; DB 4; Length 67;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
US-09-636-399A-60
Sequence 60, Application US/09636399A
Patent No. 6576755
GENERAL INFORMATION:
APPLICANT: Adler, David A.
APPLICANT: Holloway, James L.
APPLICANT: Baindur, Nand
APPLICANT: Beigel-Orme, Stephanie
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT APPLICATION NUMBER: US/09/636,399A
CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/058,335
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/636,399
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Defensin polypeptide
NAME/KEY: VARIANT
LOCATION: (33)...(33)
```

OTHER INFORMATION: Xaa is Ile, Leu, Val, Phe, or Met
US-09-636-399A-60

Query Match 30.8%; Score 20; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 YYCVRVGGRCVAVLSCLPKKE 50
|||
Db 1 YYCVRVGGRCVAVLSCLPKKE 20

RESULT 6

US-09-636-399A-58
Sequence 58, Application US/09636399A
Patent No. 6576755
GENERAL INFORMATION:
APPLICANT: Adler, David A.
APPLICANT: Holloway, James L.
APPLICANT: Baindur, Nand
APPLICANT: Beigel-Orme, Stephanie
APPLICANT: Shepherd, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT APPLICATION NUMBER: US/09/636,399A
CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/058,335
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/636,399
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 58
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Defensin polypeptide
NAME/KEY: VARIANT
LOCATION: (34)...(34)
OTHER INFORMATION: Xaa is Ile, Leu, Val, Phe, or Met
US-09-636-399A-58

Query Match 30.8%; Score 20; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 YYCVRVGGRCVAVLSCLPKKE 50
|||
Db 2 YYCVRVGGRCVAVLSCLPKKE 21

RESULT 7

US-09-636-399A-59
Sequence 59, Application US/09636399A
Patent No. 6576755
GENERAL INFORMATION:
APPLICANT: Adler, David A.
APPLICANT: Holloway, James L.
APPLICANT: Baindur, Nand
APPLICANT: Beigel-Orme, Stephanie
APPLICANT: Shepherd, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT APPLICATION NUMBER: US/09/636,399A
CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/058,335
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/064,294

PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/636,399
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 59
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Defensin polypeptide
NAME/KEY: VARIANT
LOCATION: (33)...(33)
OTHER INFORMATION: Xaa is Ile, Leu, Met, Phe, or Val
US-09-636-399A-59

Query Match 30.8%; Score 20; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 YYCVRVGGRCVAVLSCLPKKE 50
|||
Db 1 YYCVRVGGRCVAVLSCLPKKE 20

RESULT 8

US-09-636-399A-56
Sequence 56, Application US/09636399A
Patent No. 6576755
GENERAL INFORMATION:
APPLICANT: Adler, David A.
APPLICANT: Holloway, James L.
APPLICANT: Baindur, Nand
APPLICANT: Beigel-Orme, Stephanie
APPLICANT: Shepherd, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT APPLICATION NUMBER: US/09/636,399A
CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/058,335
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/636,399
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 56
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Defensin polypeptide
NAME/KEY: VARIANT
LOCATION: (35)...(35)
OTHER INFORMATION: Xaa is Ile, Leu, Val, Phe, or Met
US-09-636-399A-56

Query Match 30.8%; Score 20; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.4e-14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 YYCVRVGGRCVAVLSCLPKKE 50
|||
Db 3 YYCVRVGGRCVAVLSCLPKKE 22

RESULT 9

US-09-636-399A-57

```
/ Sequence 57, Application US/09636399A
/ Patent No. 6576755
/ GENERAL INFORMATION:
/ APPLICANT: Adler, David A.
/ APPLICANT: Holloway, James L.
/ APPLICANT: Baidur, Nand
/ APPLICANT: Beigel-Orme, Stephanie
/ APPLICANT: Sheppard, Paul O.
/ TITLE OF INVENTION: NOVEL BETA-DEFENSINS
/ FILE REFERENCE: 97-44C2
/ CURRENT APPLICATION NUMBER: US/09/636,399A
/ PRIOR FILING DATE: 2000-08-10
/ PRIOR APPLICATION NUMBER: 60/058,335
/ PRIOR FILING DATE: 1997-10-09
/ PRIOR APPLICATION NUMBER: 60/064,294
/ PRIOR FILING DATE: 1997-11-05
/ PRIOR APPLICATION NUMBER: 09/150,786
/ PRIOR FILING DATE: 1998-09-10
/ PRIOR APPLICATION NUMBER: 09/636,399
/ PRIOR FILING DATE: 2000-08-10
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 54
/ LENGTH: 39
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Defensin polypeptide
/ NAME/KEY: VARIANT
/ LOCATION: (34)...(34)
/ OTHER INFORMATION: Xaa is Ile, Leu, Val, Phe, or Met
US-09-636-399A-57

Query Match          30.8%; Score 20; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 1,4e-14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 YYCVRGGRCAVLSCLPKKE 50
DB 2 YYCVRGGRCAVLSCLPKKE 21

RESULT 10
US-09-636-399A-54
/ Sequence 54, Application US/09636399A
/ Patent No. 6576755
/ GENERAL INFORMATION:
/ APPLICANT: Adler, David A.
/ APPLICANT: Holloway, James L.
/ APPLICANT: Baidur, Nand
/ APPLICANT: Beigel-Orme, Stephanie
/ APPLICANT: Sheppard, Paul O.
/ TITLE OF INVENTION: NOVEL BETA-DEFENSINS
/ FILE REFERENCE: 97-44C2
/ CURRENT APPLICATION NUMBER: US/09/636,399A
/ PRIOR FILING DATE: 2000-08-10
/ PRIOR APPLICATION NUMBER: 60/058,335
/ PRIOR FILING DATE: 1997-10-09
/ PRIOR APPLICATION NUMBER: 60/064,294
/ PRIOR FILING DATE: 1997-11-05
/ PRIOR APPLICATION NUMBER: 09/150,786
/ PRIOR FILING DATE: 1998-09-10
/ PRIOR APPLICATION NUMBER: 09/636,399
/ PRIOR FILING DATE: 2000-08-10
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 54
/ LENGTH: 39
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Defensin polypeptide
/ NAME/KEY: VARIANT
/ LOCATION: (35)...(35)
/ OTHER INFORMATION: Xaa is Leu, Val, Ile, Met, or Phe
US-09-636-399A-55
```

```
/ LOCATION: (36)...(36)
/ OTHER INFORMATION: Xaa is Leu, Ile, Met, Phe, or Val
US-09-636-399A-54

Query Match          30.8%; Score 20; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 1,4e-14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 YYCVRGGRCAVLSCLPKKE 50
DB 4 YYCVRGGRCAVLSCLPKKE 23

RESULT 11
US-09-636-399A-55
/ Sequence 55, Application US/09636399A
/ Patent No. 6576755
/ GENERAL INFORMATION:
/ APPLICANT: Adler, David A.
/ APPLICANT: Holloway, James L.
/ APPLICANT: Baidur, Nand
/ APPLICANT: Beigel-Orme, Stephanie
/ APPLICANT: Sheppard, Paul O.
/ TITLE OF INVENTION: NOVEL BETA-DEFENSINS
/ FILE REFERENCE: 97-44C2
/ CURRENT APPLICATION NUMBER: US/09/636,399A
/ PRIOR FILING DATE: 2000-08-10
/ PRIOR APPLICATION NUMBER: 60/058,335
/ PRIOR FILING DATE: 1997-10-09
/ PRIOR APPLICATION NUMBER: 60/064,294
/ PRIOR FILING DATE: 1997-11-05
/ PRIOR APPLICATION NUMBER: 09/150,786
/ PRIOR FILING DATE: 1998-09-10
/ PRIOR APPLICATION NUMBER: 09/636,399
/ PRIOR FILING DATE: 2000-08-10
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 55
/ LENGTH: 39
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Defensin polypeptide
/ NAME/KEY: VARIANT
/ LOCATION: (35)...(35)
/ OTHER INFORMATION: Xaa is Leu, Val, Ile, Met, or Phe
US-09-636-399A-55

Query Match          30.8%; Score 20; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 1,4e-14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 YYCVRGGRCAVLSCLPKKE 50
DB 3 YYCVRGGRCAVLSCLPKKE 22

RESULT 12
US-09-636-399A-52
/ Sequence 52, Application US/09636399A
/ Patent No. 6576755
/ GENERAL INFORMATION:
/ APPLICANT: Adler, David A.
/ APPLICANT: Holloway, James L.
/ APPLICANT: Baidur, Nand
/ APPLICANT: Beigel-Orme, Stephanie
/ APPLICANT: Sheppard, Paul O.
/ TITLE OF INVENTION: NOVEL BETA-DEFENSINS
/ FILE REFERENCE: 97-44C2
/ CURRENT APPLICATION NUMBER: US/09/636,399A
/ PRIOR FILING DATE: 2000-08-10
/ PRIOR APPLICATION NUMBER: 60/058,335
/ PRIOR FILING DATE: 1997-10-09
```

```
/ PRIOR APPLICATION NUMBER: 60/064,294
/ PRIOR FILING DATE: 1997-11-05
/ PRIOR APPLICATION NUMBER: 09/150,786
/ PRIOR FILING DATE: 1998-09-10
/ PRIOR APPLICATION NUMBER: 09/636,399
/ PRIOR FILING DATE: 2000-08-10
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO: 52
/ LENGTH: 40
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Defensin polypeptide
/ NAME/KEY: VARIANT
/ LOCATION: (37)...(37)
/ OTHER INFORMATION: Xaa is Met, Leu, Ile, Val, or Phe
US-09-636-399A-52
```

```
Query Match          30.8%; Score 20; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1,4e-14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      31 YTCRVGRCGCAVLSCLPKEE 50
         |||||
Db       5 YTCRVGRCGCAVLSCLPKEE 24
```

```
RESULT 13
US-09-636-399A-53
/ Sequence 53, Application US/09636399A
/ Patent No. 6576755
/ GENERAL INFORMATION:
/ APPLICANT: Adler, David A.
/ APPLICANT: Holloway, James L.
/ APPLICANT: Baidur, Nand
/ APPLICANT: Beigel-Orme, Stephanie
/ APPLICANT: Sheppard, Paul O.
/ TITLE OF INVENTION: NOVEL BETA-DEFENSINS
/ FILE REFERENCE: 97-44C2
/ CURRENT APPLICATION NUMBER: US/09/636,399A
/ CURRENT FILING DATE: 2000-08-10
/ PRIOR APPLICATION NUMBER: 60/058,335
/ PRIOR FILING DATE: 1997-10-09
/ PRIOR APPLICATION NUMBER: 60/064,294
/ PRIOR FILING DATE: 1997-11-05
/ PRIOR APPLICATION NUMBER: 09/150,786
/ PRIOR FILING DATE: 1998-09-10
/ PRIOR APPLICATION NUMBER: 09/636,399
/ PRIOR FILING DATE: 2000-08-10
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO: 53
/ LENGTH: 40
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Defensin polypeptide
/ NAME/KEY: VARIANT
/ LOCATION: (36)...(36)
/ OTHER INFORMATION: Xaa is Ile, Leu, Phe, Val, or Met
US-09-636-399A-53
```

```
Query Match          30.8%; Score 20; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1,4e-14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      31 YTCRVGRCGCAVLSCLPKEE 50
         |||||
Db       4 YTCRVGRCGCAVLSCLPKEE 23
```

RESULT 14

```
US-09-636-399A-50
/ Sequence 50, Application US/09636399A
/ Patent No. 6576755
/ GENERAL INFORMATION:
/ APPLICANT: Adler, David A.
/ APPLICANT: Holloway, James L.
/ APPLICANT: Baidur, Nand
/ APPLICANT: Beigel-Orme, Stephanie
/ APPLICANT: Sheppard, Paul O.
/ TITLE OF INVENTION: NOVEL BETA-DEFENSINS
/ FILE REFERENCE: 97-44C2
/ CURRENT APPLICATION NUMBER: US/09/636,399A
/ CURRENT FILING DATE: 2000-08-10
/ PRIOR APPLICATION NUMBER: 60/058,335
/ PRIOR FILING DATE: 1997-10-09
/ PRIOR APPLICATION NUMBER: 60/064,294
/ PRIOR FILING DATE: 1997-11-05
/ PRIOR APPLICATION NUMBER: 09/150,786
/ PRIOR FILING DATE: 1998-09-10
/ PRIOR APPLICATION NUMBER: 09/636,399
/ PRIOR FILING DATE: 2000-08-10
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO: 50
/ LENGTH: 41
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Defensin polypeptide
/ NAME/KEY: VARIANT
/ LOCATION: (38)...(38)
/ OTHER INFORMATION: Xaa is Ile, Leu, Phe, Val, or Met
US-09-636-399A-50
```

```
Query Match          30.8%; Score 20; DB 4; Length 41;
Best Local Similarity 100.0%; Pred. No. 1,5e-14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      31 YTCRVGRCGCAVLSCLPKEE 50
         |||||
Db       6 YTCRVGRCGCAVLSCLPKEE 25
```

```
RESULT 15
US-09-636-399A-51
/ Sequence 51, Application US/09636399A
/ Patent No. 6576755
/ GENERAL INFORMATION:
/ APPLICANT: Adler, David A.
/ APPLICANT: Holloway, James L.
/ APPLICANT: Baidur, Nand
/ APPLICANT: Beigel-Orme, Stephanie
/ APPLICANT: Sheppard, Paul O.
/ TITLE OF INVENTION: NOVEL BETA-DEFENSINS
/ FILE REFERENCE: 97-44C2
/ CURRENT APPLICATION NUMBER: US/09/636,399A
/ CURRENT FILING DATE: 2000-08-10
/ PRIOR APPLICATION NUMBER: 60/058,335
/ PRIOR FILING DATE: 1997-10-09
/ PRIOR APPLICATION NUMBER: 60/064,294
/ PRIOR FILING DATE: 1997-11-05
/ PRIOR APPLICATION NUMBER: 09/150,786
/ PRIOR FILING DATE: 1998-09-10
/ PRIOR APPLICATION NUMBER: 09/636,399
/ PRIOR FILING DATE: 2000-08-10
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO: 51
/ LENGTH: 41
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Defensin polypeptide
```

; NAME/KEY: VARIANT
; LOCATION: (37)...(37)
; OTHER INFORMATION: Xaa is Ile, Leu, Phe, Val, or Met
US-09-636-399A-51

Query Match 30.8%; Score 20; DB 4; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.5e-14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 YYCRVGGRCAYLSCLPKKE 50
Db 5 YYCRVGGRCAYLSCLPKKE 24

Search completed: October 13, 2004, 15:01:54
Job time : 38 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 14:47:19 ; Search time 158 Seconds

(without alignments)
147.579 Million cell updates/sec

Title: US-10-272-121-2

Perfect score: 65

Sequence: 1.MRIHYLFLALLFLVLPVPG.....LPKEQIGKSTRGRKCCR 65

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

A_Geneseq_23sep04:*

- 1: geneeqp1980s:*
- 2: geneeqp1990s:*
- 3: geneeqp2000s:*
- 4: geneeqp2001s:*
- 5: geneeqp2002s:*
- 6: geneeqp2003as:*
- 7: geneeqp2003bs:*
- 8: geneeqp2004s:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	100.0	65	2	AAV07243 Beta-defe
2	65	100.0	67	2	AAV07243 Beta-defe
3	65	100.0	67	3	AAAB10602 Human SAP
4	65	100.0	67	5	AAU09707 Human bet
5	65	100.0	67	5	AAU091016 Transplan
6	65	100.0	67	5	AAU091036 Transplan
7	65	100.0	67	5	AAU091036 Transplan
8	65	100.0	67	8	ADN05995 Antipsori
9	65	100.0	67	8	ADN05995 Antipsori
10	65	100.0	67	8	ADN05995 Antipsori
11	65	100.0	67	8	ADN05995 Antipsori
12	65	100.0	67	8	ADN05995 Antipsori
13	65	100.0	67	8	ADN05995 Antipsori
14	65	100.0	67	8	ADN05995 Antipsori
15	65	100.0	67	8	ADN05995 Antipsori
16	65	100.0	67	8	ADN05995 Antipsori
17	65	100.0	67	8	ADN05995 Antipsori
18	65	100.0	67	8	ADN05995 Antipsori
19	65	100.0	67	8	ADN05995 Antipsori
20	65	100.0	67	8	ADN05995 Antipsori
21	65	100.0	67	8	ADN05995 Antipsori
22	65	100.0	67	8	ADN05995 Antipsori
23	65	100.0	67	8	ADN05995 Antipsori
24	65	100.0	67	8	ADN05995 Antipsori
25	65	100.0	67	8	ADN05995 Antipsori

26	22	33.8	24	5	AAO17774 Human bet
27	19	29.2	19	5	AAO17770 Human bet
28	17	26.2	17	5	AAO17771 Human bet
29	17	26.2	17	5	AAO17770 Human bet
30	9	13.8	9	5	AAW49573 Human bet
31	9	13.8	63	4	AAE02126 Mouse bet
32	9	13.8	63	4	AAE02122 Mouse bet
33	8	12.3	5	5	AAO17769 Human bet
34	8	12.3	35	6	ABR43503 Mouse bet
35	8	12.3	63	4	ABG29228 Novel hum
36	7	10.8	86	4	ABG29228 Novel hum
37	7	10.8	99	6	ABO15026 Human NOV
38	7	10.8	106	3	AAAB24085 Human PRO
39	7	10.8	125	3	AAAB24086 Human PRO
40	7	10.8	125	3	AAAB50995 Human PRO
41	7	10.8	125	8	AD103911 Human oxy
42	7	10.8	203	7	ADDE5548 Rat Prote
43	7	10.8	219	7	ADD48307 Rat Prote
44	7	10.8	219	7	ADD48311 Rat Prote
45	7	10.8	229	4	ABG20028 Novel hum

ALIGNMENTS

RESULT 1.
ID AAV07243 standard; protein; 65 AA.
XX
AC AAV07243;
XX 06-JUL-1999 (first entry)
XX
DE Beta-defensin family member zamp1.
XX
KW Human; zamp1; beta-defensin; bacterium; fungus; virus; inflammation;
KW tissue damage; immune response; AIDS; chemotherapy; melanocortin;
KW antibody; ion flux; cytotoxic activity; mammalian cell.
XX
OS Homo sapiens.
XX
PN WC9913080-A1.
PD 16-MAR-1999.
XX
PF 10-SEP-1998; 98MO-US019222.
XX
PR 10-SEP-1997; 97US-0058335P.
PR 10-SEP-1997; 97US-00926529.
PR 05-NOV-1997; 97US-0064284P.
PR 05-NOV-1997; 97US-00964687.
XX
PA (ZYMO) ZYMOGENETICS INC.
PI Adler D, Holloway JL, Bairdur N, Beigel S;
XX WPI; 1999-215064/18.
DR N-PSDB; AAX29985.
XX
PT New zamp1 polypeptide and polynucleotide, human beta-defensins - useful
PT as diagnostic reagents and for treatment of microbial infections, and
XX AIDS.
XX
PS Claim 1; Page 70; 79pp; English.
XX
CC This sequence represents the human zamp1 protein which is a member of the
CC beta-defensin protein family. Zamp1 protein is useful as a pharmaceutical
CC composition, useful for treatment of e.g. bacterial, fungal and viral
CC infections. They are also useful pro-inflammatory, for treating chronic
CC tissue damage, and for stimulating the immune response, for treatment of
CC AIDS or chemotherapy patients. Zamp1 polypeptides and antibodies are
CC useful for studying activity of the melanocortin family; studying ion
CC flux in cell culture, and studying cytotoxic activity against mammalian

CC cells in culture, by incubation with the cells. Zamp1 polypeptides are
CC especially useful for studying epithelial defensin induction in cell
CC culture when exposed to pathogenic stimuli

XX Sequence 65 AA;

Query Match 100.0%; Score 65; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.9e-60;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLFVPGHGIIINTLQKYYCRVGRCAVLSCLPKRQIGKSTRGR 60
DB 1 MRIHYLLFALLFLFVPGHGIIINTLQKYYCRVGRCAVLSCLPKRQIGKSTRGR 60
QY 61 KCCR 65
DB 61 KCCR 65

RESULT 2

AA07244
ID AA07244 standard; protein; 67 AA.

XX AA07244;

XX 06-JUL-1999 (first entry)

XX Beta-defensin family member zamp1.

XX Human; zamp1; beta-defensin; bacterium; fungus; virus; inflammation;
XX tissue damage; immune response; AIDS; chemotherapy; melanocortin;
XX antibody; ion flux; cytotoxic activity; mammalian cell.

XX Homo sapiens.

XX WO9913080-A1.

XX 18-MAR-1999.

XX 10-SEP-1998; 98WO-US019222.

XX 10-SEP-1997; 97US-0056335P.

XX 10-SEP-1997; 97US-00926529.

XX 05-NOV-1997; 97US-0064294P.

XX 05-NOV-1997; 97US-00964687.

XX (ZIMO) ZIMOGNETICS INC.

XX Adler D, Holloway JL, Balindur N, Beigel S;

XX WPI; 1999-215064/18.

XX N-PSDB; AAX29986.

XX New zamp1 polypeptide and polynucleotide, human beta-defensins - useful
XX as diagnostic reagents and for treatment of microbial infections, and
XX AIDS.

XX Claim 1; Page 73; 79pp; English.

XX This sequence represents the human zamp1 protein which is a member of the
XX beta-defensin protein family. Zamp1 protein is useful as a pharmaceutical
XX composition, useful for treatment of e.g. bacterial, fungal and viral
XX infections. They are also useful pro-inflammatory, for treating chronic
XX tissue damage, and for stimulating the immune response, for treatment of
XX AIDS or chemotherapy patients. Zamp1 polypeptides and antibodies are
XX useful for studying activity of the melanocortin family, studying ion
XX flux in cell culture, and studying cytotoxic activity against mammalian
XX cells in culture, by incubation with the cells. Zamp1 polypeptides are
XX especially useful for studying epithelial defensin induction in cell
XX culture when exposed to pathogenic stimuli

XX Sequence 67 AA;

XX

XX

XX

XX

Query Match 100.0%; Score 65; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 1.9e-60;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLFVPGHGIIINTLQKYYCRVGRCAVLSCLPKRQIGKSTRGR 60
DB 1 MRIHYLLFALLFLFVPGHGIIINTLQKYYCRVGRCAVLSCLPKRQIGKSTRGR 60

QY 61 KCCR 65

DB 61 KCCR 65

RESULT 3

AA010602
ID AA010602 standard; protein; 67 AA.

XX AA010602;

XX 08-JAN-2001 (first entry)

XX Human SAP-3 pre-protein.

XX SAP-2; SAP-3; human; antibiotic; antibacterial; antifungal; antiviral;
XX treatment; microbial infection; wound dressing; diagnostic reagent.

XX Homo sapiens.

XX WO200046245-A2.

XX 10-AUG-2000.

XX 01-FEB-2000; 2000WO-EP000776.

XX 01-FEB-1999; 99DE-01005128.

XX 08-OCT-1999; 99DE-0104936.

XX (SCHD) SCHERING AG;

XX Christophers E, Harder J, Schroeder J;

XX WPI; 2000-514948/46.

XX N-PSDB; AAX71755.

XX New human antibiotic peptides, useful for treating microbial infections,
XX particularly when incorporated in wound dressings, also related nucleic
XX acid.

XX Claim 4; Page 39; 41pp; German.

XX This invention describes the novel active, mature human proteins (I) SAP-
XX 2 and SAP-3 which have antibiotic, antibacterial, antifungal and
XX antiviral activity. (I), and their precursors, are useful for treating or
XX preventing microbial infections (caused by bacteria, fungi or viruses),
XX particularly where they (or human cells expressing them) are included in
XX wound dressings, and to produce specific antibodies (Ab) or their
XX fragments. Ab are used as diagnostic reagents, e.g. to detect a
XX deficiency of (I) or the presence of a (I) variant. This sequence
XX represents the human SAP-3 protein described in the method of the
XX invention

XX Sequence 67 AA;

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Db 61 KCCR 65

RESULT 4

AAU09707 standard; protein; 67 AA.

AAU09707;

26-MAR-2002 (first entry)

Human beta-defensin-3 (HBD-3).

Human; antimicrobial peptide; human beta-defensin-3; HBD-3; microbial growth; microbial infection; pulmonary infection.

Homo sapiens.

WO200192309-A2.

06-DEC-2001.

01-JUN-2001; 2001WO-US018057.

01-JUN-2000; 2000US-0208792P.

(IOWA) UNIV IOWA RES FOUND.

McCraty PB, Tack B, Jia HP, Schutte BC;

WPI: 2002-106302/14.

N-PSDB; AAS14407.

New human beta-defensin 3 peptides and nucleic acids encoding peptides, useful for treating or preventing microbial growth or infection, or in gene therapy.

Claim 1; Page 96; 110pp; English.

The present invention relates to the isolation of a novel antimicrobial peptide, human beta-defensin-3 (HBD-3). Also described is a method of inhibiting growth of a microbe by introducing into a host or environment the antimicrobial peptide of the invention. The peptide is useful for treating or preventing microbial growth or infections, e.g. pulmonary infections when administered by inhalation. The peptide can be applied on a work surface or a surgical instrument for the prevention and/or suppression of microbial growth. The present sequence represents HBD-3

SQ Sequence 67 AA;

Query Match 100.0%; Score 65; DB 5; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.9e-60; Mismatches 0; Gaps 0;

Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRHYLFLALFLVVPVPGHGIINTLQKYYCVRVGRCAVSLCPKEQIGKSTRGR 60

Db 1 MRHYLFLALFLVVPVPGHGIINTLQKYYCVRVGRCAVSLCPKEQIGKSTRGR 60

QY 61 KCCR 65

Db 61 KCCR 65

RESULT 5

AAU91016 standard; peptide; 67 AA.

AAU91016;

05-JUN-2002 (first entry)

Transplant media associated defensin peptide #17.

KM Transplant; antimicrobial peptide; pore forming agent;
 KM cell surface receptor binding compound; kidney transplant; cardioplegia;
 KM organ transplant; transplant rejection; defensin.

Homo sapiens.

WO200209738-A1.

27-JUL-2001; 2001WO-US023785.

28-JUN-2000; 2000US-0221632P.

17-NOV-2000; 2000US-0249602P.

15-MAY-2001; 2001US-0290932P.

(MURP/) MURPHY C J.

Murphy CJ, Reid TW, Meanlty JF;

WPI: 2002-268995/31.

Media comprising antimicrobial polypeptides or pore forming agents and/or cell surface receptor binding compounds useful for the storage and preservation of organs prior to transplant.

Claim 8; Page 28; 78pp; English.

The invention describes new transplant compositions comprising antimicrobial polypeptides or pore forming agents and/or cell surface receptor binding compounds. The media is capable of extending the preservation period past 72 hours and can provide organs with increased functionality upon transplant. Animals receiving kidneys stored in the media of the present invention for either three or four days had serum creatinine levels of less than half of those observed in control animals receiving kidneys stored in UW solution (defined in the specification) alone. Lower serum creatinine levels are indicative of healthier kidneys and a more preferable prognosis for the transplant patient. The media of the invention are useful for decreasing the incidence and/or severity of the delayed graft function in patients receiving transplanted kidneys stored and/or treated in the media. The media may also be used in procedures such as cardioplegia. It is contemplated that transplant of healthier organs leads to a decrease in chronic rejection. This sequence represents an antimicrobial defensin peptide studied in the development of the transplant media

SQ Sequence 67 AA;

Query Match 100.0%; Score 65; DB 5; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.9e-60; Mismatches 0; Gaps 0;

Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRHYLFLALFLVVPVPGHGIINTLQKYYCVRVGRCAVSLCPKEQIGKSTRGR 60

Db 1 MRHYLFLALFLVVPVPGHGIINTLQKYYCVRVGRCAVSLCPKEQIGKSTRGR 60

QY 61 KCCR 65

Db 61 KCCR 65

RESULT 6

AAU91036 standard; peptide; 67 AA.

AAU91036;

05-JUN-2002 (first entry)

Transplant media associated defensin peptide #37.

Transplant; antimicrobial peptide; pore forming agent;

cell surface receptor binding compound; kidney transplant; cardioplegia;

KM organ transplant; transplant rejection; defensin.
 XX Homo sapiens.
 OS
 XX WO200209738-A1.
 PN
 XX 07-FEB-2002.
 PD
 XX 27-JUL-2001; 2001WO-US023785.
 PF
 XX 28-JUL-2000; 2000US-0221632P.
 PR 17-NOV-2000; 2000US-0249602P.
 PR 15-MAY-2001; 2001US-0290932P.
 XX
 XX (MURP/) MURPHY C J.
 XX
 XX Murphy CJ, Reid TW, Mcanulty JF;
 PI
 XX WPI; 2002-268995/31.
 DR
 XX Media comprising antimicrobial polypeptides or pore forming agents and/or
 PT cell surface receptor binding compounds useful for the storage and
 PT preservation of organs prior to transplant.
 XX
 XX Claim 6; Page 30; 78pp; English.
 PS
 XX The invention describes new transplant compositions comprising
 CC antimicrobial polypeptides or pore forming agents and/or cell surface
 CC receptor binding compounds. The media is capable of extending the
 CC preservation period past 72 hours and can provide organs with increased
 CC functionality upon transplant. animals receiving kidneys stored in the
 CC media of the present invention for either three or four days had serum
 CC creatinine levels of less than half of those observed in control animals
 CC receiving kidneys stored in UW solution (defined in the specification)
 CC alone. Lower serum creatinine levels are indicative of healthier kidneys
 CC and a more preferable prognosis for the transplant patient. The media of
 CC the invention are useful for decreasing the incidence and/or severity of
 CC delayed graft function in patients receiving transplanted kidneys stored
 CC and/or treated in the media. The media may also be used in procedures
 CC such as cardioplegia. It is contemplated that transplant of healthier
 CC organs leads to a decrease in chronic rejection. This sequence represents
 CC an antimicrobial defensin peptide studied in the development of the
 CC transplant media
 XX
 SQ Sequence 67 AA;
 Query Match 100.0%; Score 65; DB 5; Length 67;
 Best Local Similarity 100.0%; Pred. No. 1.9e-60;
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRLHYLLFALLFLFLVYPVGHGIIINTLQKYYCRVRGRCAYLSCLPKREQIGKSTRGR 60
 DB 1 MRLHYLLFALLFLFLVYPVGHGIIINTLQKYYCRVRGRCAYLSCLPKREQIGKSTRGR 60
 QY 61 KCCRR 65
 DB 61 KCCRR 65
 DB
 RESULT 7
 ID AAO17768 standard; protein; 67 AA.
 XX
 XX AAO17768;
 AC
 XX 30-AUG-2002 (first entry)
 DT
 XX Human beta-defensin-3 derivative #3.
 DE
 XX Human; beta-defensin-3; hBD-3; bacterial infection; gene therapy;
 KM respiratory system; cystic fibrosis; inflammation; urogenital tract;
 KM antibacterial; fungicide; cytostatic; antiinflammatory; anticancer;
 KM gastrointestinal tract; septicemia; apoptosis induction; cancer.

XX Homo sapiens.
 OS
 XX WO2002040512-A2.
 PN
 XX 23-MAY-2002.
 PD
 XX 14-NOV-2001; 2001WO-EP033174.
 PF
 XX 14-NOV-2000; 2000DE-01056365.
 PR 30-MAR-2001; 2001DE-01016220.
 XX
 XX (IPFP-) IPF PHARM GMBH.
 PA
 PI Forsmann W, Kluver E, Conejo-Garcia J, Adermann K, Bals R;
 PI Maegerle H;
 PI WPI; 2002-435959/46.
 DR
 XX New human beta-defensin 3, useful for treating or preventing microbial
 PT infection and tumors, also related nucleic acid.
 PT
 XX Claim 2; Page 23; 36pp; German.
 PS
 XX The present invention relates to human beta-defensin-3 (hBD-3) and its
 CC derivatives. The peptide, its coding sequence and vectors containing the
 CC coding sequence are useful in (gene) therapy and diagnosis, especially
 CC for preventing or treating a wide range of microbial infections
 CC (particularly Burkholderia cepacia and Pseudomonas aeruginosa in the
 CC respiratory tract, especially in cases of cystic fibrosis, and
 CC Helicobacter pylori, also inflammatory diseases of the gastrointestinal
 CC and urogenital tracts, sepsis and yeast infections), and for inducing
 CC apoptosis for treating malignant melanoma and tumours. The present
 CC sequence is a derivative of human BD-3
 XX
 SQ Sequence 67 AA;
 Query Match 100.0%; Score 65; DB 5; Length 67;
 Best Local Similarity 100.0%; Pred. No. 1.9e-60;
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRLHYLLFALLFLFLVYPVGHGIIINTLQKYYCRVRGRCAYLSCLPKREQIGKSTRGR 60
 DB 1 MRLHYLLFALLFLFLVYPVGHGIIINTLQKYYCRVRGRCAYLSCLPKREQIGKSTRGR 60
 QY 61 KCCRR 65
 DB 61 KCCRR 65
 DB
 RESULT 8
 ID ADN05995 standard; protein; 67 AA.
 XX
 XX ADN05995;
 AC
 XX 01-JUL-2004 (first entry)
 DT
 XX Antipsoriatic protein sequence #1157.
 DE
 XX antipsoriatic; gene therapy; psoriasis; diagnosis.
 KM
 XX Homo sapiens.
 OS
 XX WO2004028479-A2.
 PN
 XX 08-APR-2004.
 PD
 XX 25-SEP-2003; 2003WO-US030907.
 PF
 XX 25-SEP-2002; 2002US-0414006P.
 PR
 XX (GETH) GENENTECH INC.

XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
 PI Wu TD;
 XX WPI; 2004-305105/28.
 DR N-PSDB; ADN05994.
 XX
 PT New PRO nucleic acid or polypeptide, useful for preparing a
 PT pharmaceutical composition for diagnosing or treating psoriasis in a
 PT mammal.
 PS Claim 9; SEQ ID NO 2390; 3065pp; English.
 CC The invention relates to novel polynucleotide and polypeptides for
 CC treating psoriasis or a sequence having at least 80% identity to the
 CC above sequences. The nucleic acid is useful for preparing a composition
 CC for diagnosing or treating psoriasis in a mammal. This sequence
 CC corresponds to one of the polypeptides of the invention.
 XX
 SQ Sequence 67 AA;

Query Match 100.0%; Score 65; DB 8; Length 67;
 Best Local Similarity 100.0%; Pred. No. 1.9e-60;
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRHIVLFLFLFPLVPGHGGIINTLQKYCRVGRGCAVLSCLPKESQIGKSTRGR 60
 DB 1 MRHIVLFLFLFPLVPGHGGIINTLQKYCRVGRGCAVLSCLPKESQIGKSTRGR 60
 QY 61 KCCRR 65
 DB 61 KCCRR 65

RESULT 9
 ADQ08006
 ID ADQ08006 standard; protein; 67 AA.
 AC ADQ08006;
 DT 23-SEP-2004 (first entry)
 DE Human beta-defensin-3, HBD-3, SEQ ID 15.
 XX
 KM Anti-HIV; Vaccine; HIV infection; Beta Defensin; BD; human; HBD; HBD-2;
 KM HBD-3; antiviral.
 XX
 OS Homo sapiens.
 XX
 PN WO2004054603-A2.
 PD 01-JUL-2004.
 XX
 PF 15-DEC-2003; 2003WO-US040233.
 XX
 PR 13-DEC-2002; 2002US-0433099P.
 XX
 PA (UYCA-) UNIV CASE WESTERN RESERVE.
 XX
 PI Weinberg A;
 XX
 DR WPI; 2004-488004/46.
 DR N-PSDB; ADQ08007, ADQ08008, ADQ08009.
 XX
 PT Inhibiting HIV infection in a subject comprises administering human Beta
 PT defensin-2 or human Beta defensin-3 agent or Beta Defensin-inducing
 PT agent.
 XX
 PS Claim 9; Page 10; 63pp; English.
 CC The present invention relates to a method for inhibiting HIV infection in
 CC a subject. The method comprises administering Beta Defensin (BD) agent or
 CC Beta Defensin-inducing agent e.g. a human BD (HBD) agent such as HBD-2 or

CC HBD-3. The agent is administered in combination with an additional
 CC antiviral agent which targets a portion of the HIV virus consisting of an
 CC HIV protease or an HIV reverse transcriptase. BD are a superfamily of
 CC peptide antibiotics with a characteristic beta-sheet structure stabilised
 CC by two to three intramolecular disulfide bonds. The present sequence is
 CC HBD-3.
 XX
 SQ Sequence 67 AA;

Query Match 100.0%; Score 65; DB 8; Length 67;
 Best Local Similarity 100.0%; Pred. No. 1.9e-60;
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRHIVLFLFLFPLVPGHGGIINTLQKYCRVGRGCAVLSCLPKESQIGKSTRGR 60
 DB 1 MRHIVLFLFLFPLVPGHGGIINTLQKYCRVGRGCAVLSCLPKESQIGKSTRGR 60
 QY 61 KCCRR 65
 DB 61 KCCRR 65

RESULT 10
 AAB10600
 ID AAB10600 standard; protein; 45 AA.

AC AAB10600;
 DT 08-JAN-2001 (first entry)

DE Human SAP-3 mature protein.

KM SAP-2; SAP-3; human; antibiotic; antibacterial; antifungal; antiviral;
 KM treatment; microbial infection; wound dressing; diagnostic reagent.

OS Homo sapiens.

PN WO200406245-A2.

PD 10-AUG-2000.

PF 01-FEB-2000; 2000WO-EP000776.

PR 01-FEB-1999; 99DE-01005128.

PR 08-OCT-1999; 99DE-01049436.

PA (SCHD) SCHERING AG.

PI Christophers E, Harder J, Schroeder J;

XX WPI; 2000-514948/46.

DR N-PSDB; AAA71753.

PT New human antibiotic peptides, useful for treating microbial infections,
 PT particularly when incorporated in wound dressings, also related nucleic
 PT acid.

PS Claim 1; Page 37; 41pp; German.

CC This invention describes the novel active, mature human proteins (I) SAP-
 CC 2 and SAP-3 which have antibiotic, antibacterial, antifungal and
 CC antiviral activity. (I), and their precursors, are useful for treating or
 CC preventing microbial infections (caused by bacteria, fungi or viruses),
 CC particularly where they (or human cells expressing them) are included in
 CC wound dressings, and to produce specific antibodies (Ab) or their
 CC fragments. Ab are used as diagnostic reagents, e.g. to detect a
 CC deficiency of (I) or the presence of a (I) variant. This sequence
 CC represents the mature human SAP-3 protein described in the method of the
 CC invention

SQ Sequence 45 AA;

Query Match 66.2%; Score 43; DB 3; Length 45;

Best Local Similarity 100.0%; Pred. No. 1.9e-37;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GIINTLQKYYCRVGRGCAVLSCLPKKEQIGKSTGRKCCR 65
DB 1 GIINTLQKYYCRVGRGCAVLSCLPKKEQIGKSTGRKCCR 43

RESULT 11

ID AAU09709 standard; protein; 45 AA.

XX AAU09709;

DT 26-MAR-2002 (first entry)

XX Human beta-defensin-3 (HBD-3) mature protein sequence #2.

XX Human; antimicrobial peptide; human beta-defensin-3; HBD-3;
XX microbial growth; microbial infection; pulmonary infection.

OS Homo sapiens.

PN WO200192309-A2.

XX WO200192309-A2.

PD 06-DEC-2001.

PF 01-JUN-2001; 2001WO-US018057.

PR 01-JUN-2000; 2000US-0208792P.

XX (IOWA) UNIV IOWA RES FOUND.

XX McCray PB, Tack B, Jia HP, Schutte BC;

DR WPI; 2002-106302/14.

PT New human beta-defensin 3 peptides and nucleic acids encoding peptides,
PT useful for treating or preventing microbial growth or infection, or in
PT gene therapy.

XX Claim 29; Page 98; 110pp; English.

XX The present invention relates to the isolation of a novel antimicrobial
XX peptide, human beta-defensin-3 (HBD-3). Also described is a method of
XX inhibiting growth of a microbe by introducing into a host or environment
XX the antimicrobial peptide of the invention. The peptide is useful for
XX treating or preventing microbial growth or infections, e.g. pulmonary
XX infections when administered by inhalation. The peptide can be applied on
XX a work surface or a surgical instrument for the prevention and/or
XX suppression of microbial growth. The present sequence represents HBD-3
XX mature protein sequence #2

XX Sequence 45 AA;

QY 23 GIINTLQKYYCRVGRGCAVLSCLPKKEQIGKSTGRKCCR 65

DB 1 GIINTLQKYYCRVGRGCAVLSCLPKKEQIGKSTGRKCCR 43

RESULT 12

ID AA017767 standard; peptide; 45 AA.

XX AA017767;

DT 30-AUG-2002 (first entry)

XX Human beta-defensin-3 derivative #2.

XX Human beta-defensin-3 (HBD-3) mature protein sequence #1.

XX Human; antimicrobial peptide; human beta-defensin-3; HBD-3;
XX microbial growth; microbial infection; pulmonary infection.

OS Homo sapiens.

PN WO200192309-A2.

XX WO200192309-A2.

PD 06-DEC-2001.

PF 01-JUN-2001; 2001WO-US018057.

PR 01-JUN-2000; 2000US-0208792P.

XX Human; beta-defensin-3, hbd-3; bacterial infection; gene therapy;
XX respiratory system; cystic fibrosis; inflammation; urogenital tract;
XX antibacterial; fungicide; cytostatic; anti-inflammatory; antitumor;
XX gastrointestinal tract; septicemia; apoptosis induction; cancer.

OS Homo sapiens.

PN WO200240512-A2.

XX WO200240512-A2.

PD 23-MAR-2002.

PF 14-NOV-2001; 2001WO-EP013174.

PR 14-NOV-2000; 2000DE-01056365.

XX 30-MAR-2001; 2001DE-01016220.

PA (IPPP-) IPF PHARM GMBH.

XX Forsmann W, Kluever E, Conejo-Garcia J, Adermann K, Bals R;
XX Maeger H;

DR WPI; 2002-435959/46.

XX WPI; 2002-435959/46.

PT New human beta-defensin 3, useful for treating or preventing microbial
PT infection and tumors, also related nucleic acid.

XX Claim 2; Page 23; 36pp; German.

XX The present invention relates to human beta-defensin-3 (hbd-3) and its
XX derivatives. The peptide, its coding sequence and vectors containing the
XX coding sequence are useful in (gene) therapy and diagnosis, especially
XX for preventing or treating a wide range of microbial infections
XX (particularly Burkholderia cepacia and pseudomonas aeruginosa in the
XX respiratory tract, especially in cases of cystic fibrosis, and
XX Helicobacter pylori, also inflammatory diseases of the gastrointestinal
XX and urogenital tracts, sepsis and yeast infections), and for inducing
XX apoptosis for treating malignant melanoma and tumors. The present
XX sequence is a derivative of human BD-3

XX Sequence 45 AA;

QY 23 GIINTLQKYYCRVGRGCAVLSCLPKKEQIGKSTGRKCCR 65

DB 1 GIINTLQKYYCRVGRGCAVLSCLPKKEQIGKSTGRKCCR 43

RESULT 13

ID AAU09708 standard; protein; 41 AA.

XX AAU09708;

DT 26-MAR-2002 (first entry)

XX Human beta-defensin-3 (HBD-3) mature protein sequence #1.

XX Human; antimicrobial peptide; human beta-defensin-3; HBD-3;
XX microbial growth; microbial infection; pulmonary infection.

OS Homo sapiens.

PN WO200192309-A2.

XX WO200192309-A2.

PD 06-DEC-2001.

PF 01-JUN-2001; 2001WO-US018057.

XX 01-JUN-2000; 2000US-0208792P.

XX (IOWA) UNIV IOWA RES FOUND.
 PA
 XX
 PI McCreary PB, Tack B, Jia HP, Schutte BC,
 XX
 DR WPI; 2002-106302/14.
 XX
 PT New human beta-defensin 3 peptides and nucleic acids encoding peptides,
 PT useful for treating or preventing microbial growth or infection, or in
 PT gene therapy.
 XX
 PS Claim 28; Page 97; 110pp; English.
 XX
 CC The present invention relates to the isolation of a novel antimicrobial
 CC peptide, human beta-defensin-3 (HBD-3). Also described is a method of
 CC inhibiting growth of a microbe by introducing into a host or environment
 CC the antimicrobial peptide of the invention. The peptide is useful for
 CC treating or preventing microbial growth or infections, e.g. pulmonary
 CC infections when administered by inhalation. The peptide can be applied on
 CC a work surface or a surgical instrument for the prevention and/or
 CC suppression of microbial growth. The present sequence represents HBD-3
 CC mature protein sequence #1
 CC
 SQ Sequence 41 AA;
 Query Match 60.0%; Score 39; DB 5; Length 41;
 Best Local Similarity 100.0%; Pred. No. 2.6e-33;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 27 TLQKYYCRVGRGRCVAVLSCLPKKEQIGKSTGRKCCR 65
 Db 1 TLQKYYCRVGRGRCVAVLSCLPKKEQIGKSTGRKCCR 39
 RESULT 14
 AA017766
 ID AA017766 standard; peptide; 40 AA.
 XX
 AC AA017766;
 XX
 DT 30-AUG-2002 (first entry)
 XX
 DE Human beta-defensin-3 derivative #1.
 XX
 KW Human; beta-defensin-3; hbd-3; bacterial infection; gene therapy;
 KW respiratory system; cystic fibrosis; inflammation; urogenital tract;
 KW antibacterial; fungicide; cytostatic; antiinflammatory; antitumor;
 KW gastrointestinal tract; septicemia; apoptosis induction; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200240512-A2.
 XX
 PD 23-MAY-2002.
 XX
 PF 14-NOV-2001; 2001WO-EP013174.
 XX
 PR 14-NOV-2001; 2000DE-01056365.
 PR 30-MAR-2001; 2001DE-01016220.
 XX
 PA (IFPP-) IFF PHARM GMBH.
 XX
 PI Fortsmann W, Kluever E, Conejo-Garcia J, Adermann K, Bals R,
 PI Maegert H;
 XX
 DR WPI; 2002-435959/46.
 XX
 PT New human beta-defensin 3, useful for treating or preventing microbial
 PT infection and tumors, also related nucleic acid.
 XX
 PS Claim 2; Page 23; 36pp; German.
 CC The present invention relates to human beta-defensin-3 (HBD-3) and its

CC derivatives. The peptide, its coding sequence and vectors containing the
 CC coding sequence are useful in (gene) therapy and diagnosis, especially
 CC for preventing or treating a wide range of microbial infections
 CC (particularly Burkholderia cepacia and Pseudomonas aeruginosa in the
 CC respiratory tract, especially in cases of cystic fibrosis, and
 CC Helicobacter pylori, also inflammatory diseases of the gastrointestinal
 CC and urogenital tracts, sepsis and yeast infections), and for inducing
 CC apoptosis for treating malignant melanoma and tumours. The present
 CC sequence is a derivative of human BD-3
 XX
 SQ Sequence 40 AA;
 Query Match 58.5%; Score 38; DB 5; Length 40;
 Best Local Similarity 100.0%; Pred. No. 3.1e-32;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 28 LQKYYCRVGRGRCVAVLSCLPKKEQIGKSTGRKCCR 65
 Db 1 LQKYYCRVGRGRCVAVLSCLPKKEQIGKSTGRKCCR 38
 RESULT 15
 ABR43502
 ID ABR43502 standard; peptide; 35 AA.
 XX
 AC ABR43502;
 XX
 DT 16-JUL-2003 (first entry)
 XX
 DE Human beta-defensin peptide DEFB3 SEQ ID NO:7.
 XX
 KW Beta-defensin; antimicrobial; antibacterial; vaccine; gene therapy;
 KW infection; antibiotic; chromosome 8p23-p22.
 XX
 OS Homo sapiens.
 XX
 PN WO2003024992-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 23-SEP-2002; 2002WO-US030106.
 XX
 PR 21-SEP-2001; 2001US-0323991P.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 XX
 PI McCreary PB, Schutte BC, Jia HP, Casavant TL, Welch MJ;
 PI WPI; 2003-354585/33.
 XX
 DR
 XX
 PT New antimicrobial peptides, beta-defensin, useful for preventing
 PT microbial growth, for treating pulmonary infections, for reducing
 PT resistance to antimicrobials and antibiotics, and for inhibiting
 PT multidrug resistant bacteria.
 XX
 PS Claim 1; Page 78; 125pp; English.
 XX
 CC ABR43496 to ABR43577 represent beta-defensin antimicrobial peptides (I).
 CC (I) have antibacterial activity and can be used in vaccines, and in gene
 CC therapy. (I) can be used for preventing microbial growth, for treating
 CC infections (e.g. pulmonary infections), for reducing resistance to
 CC antimicrobials and antibiotics, and for inhibiting multidrug resistant
 CC bacteria. The antimicrobial peptides may be included in food
 CC preparations, pharmaceutical preparations, medicinal and pharmaceutical
 CC products, cosmetic products, hygienic products, cleaning products and
 CC cleaning agents, as well as to any material to which the peptides could
 CC be sprayed on or adhered to where inhibition of microbial growth on such
 CC material is desired. The antimicrobial peptides and nucleic acids
 CC encoding them may be used in gene therapy. ABR43578 to ABR43610 represent
 CC human beta-defensin peptides given in an example from the present
 CC invention
 XX
 SQ Sequence 35 AA;

Query Match 53.8%; Score 35; DB 6; Length 35;
Best Local Similarity 100.0%; Pred.No. 3.9e-29;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 31 YYCRVAGRGCAVLSCLPKEEQIGKSTGRKCCRR 65
Db 1 YYCRVAGRGCAVLSCLPKEEQIGKSTGRKCCRR 35

Search completed: October 13, 2004, 14:57:06
Job time : 162 secs